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OM protein - protein search, using sw model

Run on: November 25, 2003, 14:57:29 ; Search time 21 seconds

Title: US-10-034-849-2 (without alignment)

Perfect score: 4188

Sequence: 1 MTEVFFVLSSEVNGKEP.....LKASQNTLPFLAKSK 803

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : Issued_Patents_RA*
1: /cgm2_6/pdata/1/iaa/5A_COMB pep: *
2: /cgm2_6/pdata/1/iaa/5B_COMB pep: *
3: /cgm2_6/pdata/1/iaa/6A_COMB pep: *
4: /cgm2_6/pdata/1/iaa/6B_COMB pep: *
5: /cgm2_6/pdata/1/iaa/6C_COMB pep: *
6: /cgm2_6/pdata/1/iaa/backlist01.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Mary Match	Length	DB ID	Description
1	4188	100.0	803	2	US-08-207-166-4
2	4188	100.0	803	1	US-09-391-340-4
3	4188	100.0	803	1	US-09-391-340-4
4	2963.5	70.8	803	1	US-08-062-568-2
5	1563	37.3	788	2	US-08-207-166-4
6	1563	37.3	788	4	US-09-391-340-6
7	1563	37.3	788	4	US-09-391-340-6
8	1237.5	29.5	776	2	US-08-288-432-7
9	1236.5	29.5	775	1	US-07-966-278-1
10	1236.5	29.5	775	1	US-08-424-921-1
11	1236.5	29.5	775	2	US-08-535-255-1
12	1236.5	29.5	775	2	US-08-535-255-1
13	1236.5	29.5	775	4	US-09-244-889-1
14	1234.5	29.5	774	3	US-09-073-354-1
15	1234.5	29.5	774	3	US-08-656-058-1
16	1234.5	29.5	774	3	US-09-363-095-1
17	1234.5	29.5	774	3	US-09-418-027-1
18	1234.5	29.5	774	3	US-09-585-858-35
19	1216.5	29.0	773	4	US-08-575-134-12
20	1206.5	29.8	777	4	US-08-575-134-12
21	1104	26.4	779	1	US-08-366-577-2
22	1104	26.4	779	1	US-08-366-577-2
23	1104	26.4	779	5	US-08-366-577-2
24	760.5	18.2	1107	1	US-08-366-577-2
25	739.5	17.2	1107	1	US-08-366-577-2
26	739.5	17.2	1107	1	US-08-366-577-2
27	739.5	17.7	1019	2	US-08-222-715B-26

28	722.5	17.3	734	4	US-09-585-858-6	Sequence 8, Appl
29	696.5	16.6	738	4	US-09-585-858-6	Sequence 6, Appl
30	693.5	16.6	738	4	US-09-585-858-7	Sequence 7, Appl
31	693.5	16.6	738	4	US-09-585-858-11	Sequence 11, Appl
32	693.5	16.6	738	4	US-09-585-858-11	Sequence 11, Appl
33	648.5	15.5	734	4	US-09-585-858-9	Sequence 9, Appl
34	639.5	15.2	1022	1	US-08-271-364A-8	Sequence 8, Appl
35	639.5	15.2	1022	1	US-08-271-364A-8	Sequence 8, Appl
36	579.5	13.8	1462	3	US-07-792-600-31	Sequence 31, Appl
37	579.5	13.8	1462	3	US-07-792-600-31	Sequence 31, Appl
38	579.5	13.8	1462	3	US-09-157-021-31	Sequence 31, Appl
39	579.5	13.8	1462	3	US-09-157-021-31	Sequence 31, Appl
40	560.5	13.5	702	4	US-09-585-858-24	Sequence 24, Appl
41	560.5	13.5	702	4	US-09-585-858-24	Sequence 24, Appl
42	542.5	13.0	877	2	US-08-907-166-8	Sequence 8, Appl
43	542.5	13.0	877	2	US-09-391-340-8	Sequence 8, Appl
44	542.5	12.6	1026	4	US-09-252-991A-10331	Sequence 3021, A
45	542.5	12.5	1015	2	US-08-680-328-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-907-166-4 Application US/08907166
; Sequence 4, A
; Sequence 8, A
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Macher, Eric
; INVENTOR: Callen, Walter
; TITLE: METHOD FOR THE DETECTION AND IDENTIFICATION OF NOVEL POLYMERASES
; FILE REFERENCE: 09/01/027001
; CURRENT APPLICATION NUMBER: US/08/907,166
; CURRENT FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1: US-08-907-166-4
; SEQ ID NO 2: US-08-907-166-4
; SEQ ID NO 3: US-08-907-166-4
; SEQ ID NO 4: US-08-907-166-4
; TYPE: PRT
; SOURCE: Pyrolobus fumarius
US-08-907-166-4

Query Match Best Local Similarity 100.0%; Score 4188; DB 2; Length 803;
Matches 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTEVFFVLSSEVNGKEPQVITANGKSERVLLDRESPFFVALLAPADPKQVQ	60
DB	1	MTEVFFVLSSEVNGKEPQVITANGKSERVLLDRESPFFVALLAPADPKQVQ	60
QY	61	RITALSHPSPIGVDDKQKFGPRVRLVITLFAVEVRELNVGVDDVEAD	120
DB	61	RITALSHPSPIGVDDKQKFGPRVRLVITLFAVEVRELNVGVDDVEAD	120
QY	121	IFAPMVLIDHLLFFTVFAEPLNKGSPVDVYLVKSEPEPVGELAKTLPDL	180
DB	121	IFAPMVLIDHLLFFTVFAEPLNKGSPVDVYLVKSEPEPVGELAKTLPDL	180
QY	181	RILANDVNSVQSSPSPDPVIAVTDGCEVLPFASGDDKQKHFVEVYVD	240
DB	181	RILANDVNSVQSSPSPDPVIAVTDGCEVLPFASGDDKQKHFVEVYVD	240
QY	241	POLTVGNHNSPFFVLRRLGLQGLVTRVCASTPSVGHVSFQRLAVLVYA	300
DB	241	POLTVGNHNSPFFVLRRLGLQGLVTRVCASTPSVGHVSFQRLAVLVYA	300
QY	301	REHPTIKSEVAVYLVQWKSERVLLNWEHFDNDKPSPELLVARDVYATG	360
DB	301	REHPTIKSEVAVYLVQWKSERVLLNWEHFDNDKPSPELLVARDVYATG	360
QY	361	LARKLIPFAQLSTVTLPIQDGMGVGFLRLNVLTAAPKQELVNNVPEETG	420
DB	361	LARKLIPFAQLSTVTLPIQDGMGVGFLRLNVLTAAPKQELVNNVPEETG	420

QY 421. AIVLEPIAGVHENVAVLPSVSPNIMXVWGPVTLVRPGEKCGCCWAPVVRFR 480
 Db 421. AIVLEPIAGVHENVAVLPSVSPNIMXVWGPVTLVRPGEKCGCCWAPVVRFR 480
 QY 481. RCPGFFVTVLLELLEKAVKAVRMKYPFDSVEFLDERQKALVLANSGVMSG 540
 Db 481. RCPGFFVTVLLELLEKAVKAVRMKYPFDSVEFLDERQKALVLANSGVMSG 540
 QY 541. ARMYCECAKAVTANGHLLIFATNIAKRLGVYVGTGDSVFTVDPKRVNFKIKE 600
 Db 541. ARMYCECAKAVTANGHLLIFATNIAKRLGVYVGTGDSVFTVDPKRVNFKIKE 600
 QY 601. RCPGFFVTVLLELLEKAVKAVRMKYPFDSVEFLDERQKALVLANSGVMSG 660
 Db 601. RCPGFFVTVLLELLEKAVKAVRMKYPFDSVEFLDERQKALVLANSGVMSG 660
 QY 661. LKTSVNAKAVTVKRIKVELEKGVKPIKLVKNTLSKLEETVTEAPHVAAKVLMSG 720
 Db 661. LKTSVNAKAVTVKRIKVELEKGVKPIKLVKNTLSKLEETVTEAPHVAAKVLMSG 720
 QY 721. RVSPGDKGVTVVGGGHSIQAWPFVMDPSQDVTIVVHQDITPAALRLGVGFT 780
 Db 721. RVSPGDKGVTVVGGGHSIQAWPFVMDPSQDVTIVVHQDITPAALRLGVGFT 780
 QY 781. EKKLASATGQKTLFDFLAKSK 803
 Db 781. EKKLASATGQKTLFDFLAKSK 803

RESULT 2
 US-09-391-340-4
 ; Sequence 4, Application US/0931340A
 ; Patent No. 6492511
 ; APPLICANT: Callen, Walter
 ; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF NOVEL POLYMERASES
 ; FILE REFERENCE: 09010/027001
 ; CURRENT APPLICATION NUMBER: US/09/391,340A
 ; EARLIER APPLICATION NUMBER: US/08/907,166
 ; EARLIER FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 12
 ; SEQ ID NO. 4: FactSeq for Windows Version 3.0
 ; LENGTH: 803
 ; TYPE: RPT
 ; ORGANISM: Pyrobolus fumarius
 US-09-391-340-4

Query Match 100.0%; Score 4188; DB 4; Length 803;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1. MTEWVTVLLSSEVKGSEFVVIWGIANGSERVLLRSFRPVFALLAGDQVAAQ 60
 Db 1. MTEWVTVLLSSEVKGSEFVVIWGIANGSERVLLRSFRPVFALLAGDQVAAQ 60
 QY 61. RTALSRSPSPVIGVEDNKKYCPGPRVLRITVLPNREVEYFALVAGDQVAAQ 120
 Db 61. RTALSRSPSPVIGVEDNKKYCPGPRVLRITVLPNREVEYFALVAGDQVAAQ 120
 QY 61. RTALSRSPSPVIGVEDNKKYCPGPRVLRITVLPNREVEYFALVAGDQVAAQ 120
 Db 61. RTALSRSPSPVIGVEDNKKYCPGPRVLRITVLPNREVEYFALVAGDQVAAQ 120
 QY 121. IFRANVTVLIDHLPFPTVVEALPKNKGVEGVNVLKNSRPFVYKSLAPLGLDL 180
 Db 121. IFRANVTVLIDHLPFPTVVEALPKNKGVEGVNVLKNSRPFVYKSLAPLGLDL 180
 QY 181. RTALSRSPSPVIGVEDNKKYCPGPRVLRITVLPNREVEYFALVAGDQVAAQ 240
 Db 181. RTALSRSPSPVIGVEDNKKYCPGPRVLRITVLPNREVEYFALVAGDQVAAQ 240
 QY 181. RTALSRSPSPVIGVEDNKKYCPGPRVLRITVLPNREVEYFALVAGDQVAAQ 240
 Db 181. RTALSRSPSPVIGVEDNKKYCPGPRVLRITVLPNREVEYFALVAGDQVAAQ 240
 QY 241. PDIVTVNNHNPVLLRARIKLGKLVTRVVGLEFTTVGHGVSVGRLVLDVYA 300
 Db 241. PDIVTVNNHNPVLLRARIKLGKLVTRVVGLEFTTVGHGVSVGRLVLDVYA 300

Db 241. PDIVTVNNHNPVLLRARIKLGKLVTRVVGLEFTTVGHGVSVGRLVLDVYA 300
 QY 301. EMEPEFKIKSLSEVATVYQMKKSERVIVNMPVDPKRVKQVRLVAVDQVAAQ 360
 Db 301. EMEPEFKIKSLSEVATVYQMKKSERVIVNMPVDPKRVKQVRLVAVDQVAAQ 360
 QY 361. LAKIKLPIALQSVLGCPLQVGVNAGVSGVSEVYIIRAKPKVSEVTVNREVEFTYNG 420
 Db 361. LAKIKLPIALQSVLGCPLQVGVNAGVSGVSEVYIIRAKPKVSEVTVNREVEFTYNG 420
 QY 421. AIVLEPIAGVHENVAVLPSVSPNIMXVWGPVTLVRPGEKCGCCWAPVVRFR 480
 Db 421. AIVLEPIAGVHENVAVLPSVSPNIMXVWGPVTLVRPGEKCGCCWAPVVRFR 480
 QY 481. RCPGFFVTVLLELLEKAVKAVRMKYPFDSVEFLDERQKALVLANSGVMSG 540
 Db 481. RCPGFFVTVLLELLEKAVKAVRMKYPFDSVEFLDERQKALVLANSGVMSG 540
 QY 541. ARMYCECAKAVTANGHLLIFATNIAKRLGVYVGTGDSVFTVDPKRVNFKIKE 600
 Db 541. ARMYCECAKAVTANGHLLIFATNIAKRLGVYVGTGDSVFTVDPKRVNFKIKE 600
 QY 601. EKGFEIKLVKVEVTFPTAKKRVAGLGGEDIVGFEAVGDMCHLAKVQTKVIV 660
 Db 601. EKGFEIKLVKVEVTFPTAKKRVAGLGGEDIVGFEAVGDMCHLAKVQTKVIV 660
 QY 661. LKTSVNAKAVTVKRIKVELEKGVKPIKLVKNTLSKLEETVTEAPHVAAKVLMSG 720
 Db 661. LKTSVNAKAVTVKRIKVELEKGVKPIKLVKNTLSKLEETVTEAPHVAAKVLMSG 720
 QY 721. RVSPGDKGVTVVGGGHSIQAWPFVMDPSQDVTIVVHQDITPAALRLGVGFT 780
 Db 721. RVSPGDKGVTVVGGGHSIQAWPFVMDPSQDVTIVVHQDITPAALRLGVGFT 780
 QY 781. EKKLASATGQKTLFDFLAKSK 803
 Db 781. EKKLASATGQKTLFDFLAKSK 803

RESULT 3
 US-08-062-368-4
 ; Sequence 4, Application US/08062368
 ; Patent No. 6492511
 ; APPLICANT: Gelfand, David H.
 ; APPLICANT: Wang, Alice M.
 ; TITLE OF INVENTION: Polynucleotides and Related Thermostable Nucleic Acid
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: 340 Clapboard Street
 ; CITY: Nutley
 ; STATE: New Jersey
 ; COUNTRY: U.S.A.
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: PC/XT/AT/PS/2/MS-DOS
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/062,368
 ; FILING DATE: 19930514
 ; NAME: Sias Ph.D., Stacey R.
 ; ATTORNEY/AGENT INFORMATION:
 ; REGISTRATION NUMBER: 32,630
 ; TELEPHONE: (510) 814-2863
 ; TELEFAX: (510) 814-2977
 ; INFORMATION FOR SEQ ID NO. 4:
 ; Sequence 4, Application US/08062368
 ; Patent No. 6492511
 ; APPLICANT: Gelfand, David H.
 ; APPLICANT: Wang, Alice M.
 ; TITLE OF INVENTION: Polynucleotides and Related Thermostable Nucleic Acid
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: 340 Clapboard Street
 ; CITY: Nutley
 ; STATE: New Jersey
 ; COUNTRY: U.S.A.
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: PC/XT/AT/PS/2/MS-DOS
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/062,368
 ; FILING DATE: 19930514
 ; NAME: Sias Ph.D., Stacey R.
 ; ATTORNEY/AGENT INFORMATION:
 ; REGISTRATION NUMBER: 32,630
 ; TELEPHONE: (510) 814-2863
 ; TELEFAX: (510) 814-2977
 ; INFORMATION FOR SEQ ID NO. 4:

1 SEQUENCE CHARACTERISTICS:
 1 LENGTH: 803 amino acids
 1 TYPE: amino acid
 1 STRANDNESS: single
 1 LINKAGE: linear
 1 MOLECULE TYPE: DNA (genomic)
 US-08-062-368-4

Query Match 72.34; Score 3028.5; DB 1; Length 803;
 Best Local Similarity 68.4%; Pred. No. 2.3e-264;
 Matches 570; Conservative 106; Mismatches 122; Indels 7; Gaps 5;

Qy 1 MTWV-FVVLSSVWVSGSPVLIIGIAENGVRVLDISFRFPFYALLAQAQPK--SQ 57
 Db 1 MTWTFVFLSSLSLSEFPVLIAGITLSENVLDHREFPFYALLNGSVGWR 60
 Qy 58 VQARALRERKSPFIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 117
 Db 58 VQARALRERKSPFIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 117
 Qy 61 PASIRLSEVAGSPVLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 120
 Db 61 PASIRLSEVAGSPVLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 120
 Qy 118 EADIRPAMVYLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 177
 Db 118 EADIRPAMVYLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 177
 Qy 121 EADIRPAMVYLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 178
 Db 121 EADIRPAMVYLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 178
 Qy 178 PULALFPIVSVQSGSPRPVPIVAVITDQGVLFIAKCDKRPREFVEVK 237
 Db 178 PULALFPIVSVQSGSPRPVPIVAVITDQGVLFIAKCDKRPREFVEVK 237
 Qy 179 PFWLAFPIVSVQSGSPRPVPIVAVITDQGVLFIAKCDKRPREFVEVK 238
 Db 179 PFWLAFPIVSVQSGSPRPVPIVAVITDQGVLFIAKCDKRPREFVEVK 238
 Qy 238 RYDDIIVGVNNHDPVLPFLARLGITDQGVLFIAKCDKRPREFVEVK 297
 Db 238 RYDDIIVGVNNHDPVLPFLARLGITDQGVLFIAKCDKRPREFVEVK 297
 Qy 239 ADPDIIVGVNNHDPVLPFLARLGITDQGVLFIAKCDKRPREFVEVK 298
 Db 239 ADPDIIVGVNNHDPVLPFLARLGITDQGVLFIAKCDKRPREFVEVK 298
 Qy 298 DYAEWPEIKTSLSEVAVLYGWKKSERYIIMWRIPTVDQDKEPLVQADVRA 357
 Db 298 DYAEWPEIKTSLSEVAVLYGWKKSERYIIMWRIPTVDQDKEPLVQADVRA 357
 Qy 299 DYAEWPEIKTSLSEVAVLYGWKKSERYIIMWRIPTVDQDKEPLVQADVRA 358
 Db 299 DYAEWPEIKTSLSEVAVLYGWKKSERYIIMWRIPTVDQDKEPLVQADVRA 358
 Qy 358 TYGLARLIPERLQSLVWVGLDQGVNGVGRLENVLIIRAFKMLVPRVDEPT 417
 Db 358 TYGLARLIPERLQSLVWVGLDQGVNGVGRLENVLIIRAFKMLVPRVDEPT 417
 Qy 359 TYGLARLIPERLQSLVWVGLDQGVNGVGRLENVLIIRAFKMLVPRVDEPT 418
 Db 359 TYGLARLIPERLQSLVWVGLDQGVNGVGRLENVLIIRAFKMLVPRVDEPT 418
 Qy 418 YGVALVLEPLRGVNHIAVLDSSSNPNMKTKNVGDPLVPEKCGC--CGWBAPEVK 476
 Db 418 YGVALVLEPLRGVNHIAVLDSSSNPNMKTKNVGDPLVPEKCGC--CGWBAPEVK 476
 Qy 419 YGVALVLEPLRGVNHIAVLDSSSNPNMKTKNVGDPLVPEKCGC--CGWBAPEVK 478
 Db 419 YGVALVLEPLRGVNHIAVLDSSSNPNMKTKNVGDPLVPEKCGC--CGWBAPEVK 478
 Qy 477 HIFRCPGPGFTKLELLKLRVRAEMKPTPDSPEYLLDERQALKVLANNSTY 536
 Db 477 HIFRCPGPGFTKLELLKLRVRAEMKPTPDSPEYLLDERQALKVLANNSTY 536
 Qy 479 HIFRCPGPGFTKLELLKLRVRAEMKPTPDSPEYLLDERQALKVLANNSTY 538
 Db 479 HIFRCPGPGFTKLELLKLRVRAEMKPTPDSPEYLLDERQALKVLANNSTY 538
 Qy 537 GMSARVYCRCAVATVANGRHLPRTAIKRLKLVGIDKDFVTPDEKVFNIK 596
 Db 537 GMSARVYCRCAVATVANGRHLPRTAIKRLKLVGIDKDFVTPDEKVFNIK 596
 Qy 539 GMSARVYCRCAVATVANGRHLPRTAIKRLKLVGIDKDFVTPDEKVFNIK 598
 Db 539 GMSARVYCRCAVATVANGRHLPRTAIKRLKLVGIDKDFVTPDEKVFNIK 598
 Qy 597 IXKEELGPKLEKLVYLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 656
 Db 597 IXKEELGPKLEKLVYLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 656
 Qy 599 FQVTEKGLKASGQKTLVDFSLAKK 801
 Db 599 FQVTEKGLKASGQKTLVDFSLAKK 801
 Qy 657 VEIVATSEWKAAPVTKVYVLESGVPIIKVINKTSLSEVAVLYGWKKSERYI 716
 Db 657 VEIVATSEWKAAPVTKVYVLESGVPIIKVINKTSLSEVAVLYGWKKSERYI 716
 Qy 659 AEIVLTGVNKAISREIVLQKRGKVPITLIIKNTLSKSEIPEHEDAPHMAWERN 718
 Db 659 AEIVLTGVNKAISREIVLQKRGKVPITLIIKNTLSKSEIPEHEDAPHMAWERN 718
 Qy 717 LSNATVYSFOKGVVWVGGRISORAWPNVQSPQDQVTVVHQIIPALRIQY 776
 Db 717 LSNATVYSFOKGVVWVGGRISORAWPNVQSPQDQVTVVHQIIPALRIQY 776
 Qy 719 FQVTEKGLKASGQKTLVDFSLAKK 801
 Db 719 FQVTEKGLKASGQKTLVDFSLAKK 801
 Qy 777 FQVTEKGLKASGQKTLVDFSLAKK 801
 Db 777 FQVTEKGLKASGQKTLVDFSLAKK 801

RESULT 4

US-08-062-368-2

1 Sequence 2, Application US/0802348

1 Patent No. 5491086

1 GENERAL INFORMATION:
 1 APPLICANT: Galsand, David H.
 1 APPLICANT: Wang, Alice M.
 1 TITLE OF INVENTION: Purified Thermostable Nucleic Acid
 1 INVENTOR: Galsand, David H.; Wang, Alice M.
 1 NUMBER OF SEQUENCES: 1
 1 NUMBER OF SEQUENCES: 1
 1 CORRESPONDENCE ADDRESS:
 1 ADDRESSEE: Hoffmann-La Roche Inc.
 1 STREET: 340 Kingsland Street
 1 CITY: Nutley, New Jersey
 1 STATE: New Jersey
 1 COUNTRY: U.S.A.
 1 ZIP: 07110
 1 COMPUTER READABLE FORM:
 1 MEDIA TYPE: 3.5 inch disk
 1 COMPUTER: IBM PC compatible
 1 OPERATING SYSTEM: PC-DOS/MS-DOS
 1 SOFTWARE: Patent Release #1.0, Version #1.25
 1 CHECKED BY: Galsand, David H.
 1 APPLICATION NUMBER: US/08/062,368
 1 FILING DATE: 19930514
 1 CLASSIFICATION: 435
 1 ATOM/RESIDUE INFORMATION:
 1 NAME: SUGAR
 1 NUMBER: 803
 1 REGISTRATION NUMBER: 32,630
 1 REFERENCE/DOCKET NUMBER: 8584
 1 TELECOMMUNICATION INFORMATION:
 1 TELEPHONE: (910) 814-2543
 1 TELEFAX: (910) 814-2977
 1 INFORMATION FOR SEQ ID NO: 2:
 1 LENGTH: 803 amino acids
 1 TYPE: amino acid
 1 STRANDNESS: single
 1 TOPOLOGY: linear
 1 MOLECULE TYPE: DNA (genomic)
 US-08-062-368-2

Query Match 70.8%; Score 2963.5; DB 1; Length 803;
 Best Local Similarity 68.4%; Pred. No. 2.3e-264;
 Matches 551; Conservative 118; Mismatches 159; Indels 7; Gaps 5;

Qy 1 MTWV-FVVLSSVWVSGSPVLIIGIAENGVRVLDISFRFPFYALLAQAQPK--Q 57
 Db 1 MPAEIRFAMVLIQKLVYLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 117
 Qy 58 VQARALRERKSPFIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 117
 Db 61 VQARALRERKSPFIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 120
 Qy 118 EADIRPAMVYLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 177
 Db 121 EADIRPAMVYLIQVDDKRGRRPRLRTVLPFAVEFLVAVNGVDEVL 178
 Qy 178 PULALFPIVSVQSGSPRPVPIVAVITDQGVLFIAKCDKRPREFVEVK 237
 Db 179 PFWLAFPIVSVQSGSPRPVPIVAVITDQGVLFIAKCDKRPREFVEVK 238
 Qy 238 RYDDIIVGVNNHDPVLPFLARLGITDQGVLFIAKCDKRPREFVEVK 297
 Db 239 ADPDIIVGVNNHDPVLPFLARLGITDQGVLFIAKCDKRPREFVEVK 298
 Qy 298 DYAEWPEIKTSLSEVAVLYGWKKSERYIIMWRIPTVDQDKEPLVQADVRA 357
 Db 299 DYAEWPEIKTSLSEVAVLYGWKKSERYIIMWRIPTVDQDKEPLVQADVRA 358
 Qy 358 TYGLARLIPERLQSLVWVGLDQGVNGVGRLENVLIIRAFKMLVPRVDEPT 417
 Db 359 TYGLARLIPERLQSLVWVGLDQGVNGVGRLENVLIIRAFKMLVPRVDEPT 418
 Qy 418 YGVALVLEPLRGVNHIAVLDSSSNPNMKTKNVGDPLVPEKCGC--CGWBAPEVK 476
 Db 419 YGVALVLEPLRGVNHIAVLDSSSNPNMKTKNVGDPLVPEKCGC--CGWBAPEVK 478

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Qy 477 HRFRCPGFFKTVLRLKLRVAKMKYPPDSPTBLDEROKALYANASTGM 536
Db 479 HWHTSPGFFKTVLRLKLRVAKMKYPPDSPTBLDEROKALYANASTGM 538
Qy 537 QNGSGAWYCBGAGVATNGRHRTAIRTAIRKGLVIGTOSLFTVYDPEKVENFK 596
Db 539 QVHAWYCBGAGVATNGRHRTAIRTAIRKGLVIGTOSLFTVYDPEKVENFK 598
Qy 597 TIKELGFTKLEKLVFKLFTFAKRYAGLEDRIDGSEAVRGWCMCLAKRGV 656
Db 599 FVKQGLGFTKLEKLVFKLFTFAKRYAGLEDRIDGSEAVRGWCMCLAKRGV 658
Qy 599 FVKQGLGFTKLEKLVFKLFTFAKRYAGLEDRIDGSEAVRGWCMCLAKRGV 658
Db 657 FVKQGLGFTKLEKLVFKLFTFAKRYAGLEDRIDGSEAVRGWCMCLAKRGV 716
Db 659 FVKQGLGFTKLEKLVFKLFTFAKRYAGLEDRIDGSEAVRGWCMCLAKRGV 718
Qy 717 LSGAVRGVSGDGLGVIVGVGGRIQORAPYFNVGDSQIDVTVYDQIIPAALRLGY 776
Db 719 LSGAVRGVSGDGLGVIVGVGGRIQORAPYFNVGDSQIDVTVYDQIIPAALRLGY 778
Qy 777 FGLTKELKAKASQKTFPDLAK 801
Db 778 FGLTKELKAKASQKTFPDLAK 802

RESULT 5
US-08-907-166-6
/ Sequence 6, Application US/08907166
/ Best Local Similarity 41.34; Pred. No. 3.5e-135;
/ Matches 338; Conservative 154; Mismatches 273; Indels 54; Gaps 18;
/ GENERAL INFORMATION:
/ APPLICANT: Callen, Walter
/ APPLICANT: Mather, Eric
/ FILE REFERENCE: 09010/027001
/ TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF NOVEL POLYMERASES
/ CURRENT APPLICATION NUMBER: US/08/907,166
/ EARLIER FILING DATE: 1997-08-06
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ LENGTH: 788
/ TYPE: PRT
/ ORGANISM: Archaeoglobus lithotrophicus
US-08-907-166-6

Query Match 37.34; Score 1563; DB 2; Length 788;
Best Local Similarity 41.34; Pred. No. 3.5e-135;
Matches 338; Conservative 154; Mismatches 273; Indels 54; Gaps 18;
Qy 1 MTEVTVFLDSYEVVGVKQFVINGIANGERNVILDSRFRFVALLAGAPQVQAQ 60
Db 1 MTKVGMGLADITENDRAVIRLAKCKDEG-IFTADHDSFQFYALKESGTFADIVK 59
Qy 61 -RIRALSRSPTGIVGDEKSKYFGSPREVLIRITVLPEAVREVLNVQDVELEA 119
Db 60 IKQVTKWTFP-LKVEETKATNGHEVFKVIRPQVFKLREVSQ---VLEIIRA 115
Qy 120 DIRAFKLLDHLDPFTFVTVKAEPLNAGFVQKVLVK--SRPELYGELAPTKL 177
Db 116 DIPFAKLLDNLKADMGVIGVVEREK-GLCYEKLIERDSQ-----F 163
Qy 178 POLRIALDPIEVSQSGSPREPDPVIVAKTDGDFVLFASGDKDQKPIREPVVK 237
Db 164 PELKAWDCEMSVQDPDQKPIVVISKGEYEL---NGNRELLRTPKAIIR 220
Qy 238 RYDPLIVGVNNSHPVLLERAILKGLVTRVAGAPRTSVHGVNSVPEALVLY 297
Db 221 DTDIDPIVGVNNSHPVLLERAILKGLVTRVAGAPRTSVHGVNSVPEALVLY 298
Qy 298 DVASEPHITKIGSEAVYGVNWSKSEV INWSEIYMDQPKPRLLOQADVRA 357
Db 279 DTAMSLDVLKLVNASEFLG--KTLADIENDIHWTS--GDSESVTKYKSDILH 335

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Qy 358 TYGLAKLIFALQSLVGTCLPDQVCMVSFGLMPLRIFDAFQKVLNVERPBT 417
Db 336 TYFBAKLDPHTLSEMRIRPLDVTSGRGKQVMSLLESHKLCELANPREH-ADS 394
Qy 418 YGATVLEPGRGCHENINLDSQSNVIMKIVKQVDPFVFGKGGCCGCVARVH 477
Db 395 YEGAFVLEPARAGLWICLDFASPMISIMISPTLVI--GKDCDGV--APEVGH 450
Qy 478 FRCRCPGFFKTVLRLKLRVAKMKYPPDSPTBLDEROKALYANASTGM 537
Db 451 KPRGPDGFFKTVLRLKLRVAKMKYPPDSPTBLDEROKALYANASTGM 510
Qy 538 HSGAWYCBGAGVATNGRHRTAIRTAIRKGLVIGTOSLFTVYDPEKVENFK 597
Db 511 WSLAWYCBGAGVATNGRHRTAIRTAIRKGLVIGTOSLFTVYDPEKVENFK 570
Qy 598 IK-----BELGFTKLEKLVFKLFTFAKRYAGLEDRIDGSEAVRGWCMCLAK 650
Db 571 VKLGLCSLSENPQIETDEIVETIPV--KSLVAT--QKQILVKNVGRKQMLCLAK 629
Qy 651 EVQTKVETVLAKTSVKNVAVYKVKLEKGVFKTEKLVKLSKLELYETTBADV 710
Db 630 KIQGVYHILDAENGRAPETVKNVLEKAGLPEDITITKGLTRPKNYSQMAV 689
Qy 711 VAKENLSAGVRSFGDKGVIVGVGGRIQORAPYFNVGDSQIDVTVYDQIIPAALRLGY 776
Db 690 KAKKAKNGKIVYTVGKGVFNVGVNGIGDAPPSDIEDGDFGVTDLQNKYTKD 749
Qy 759 TVYDQIIPAALRLGYFGTEKKLKASATQKTFPDL 797
Db 750 EYTDHVLPSVRLERPGTFAQKGNAS-QTLDAP 787

RESULT 6
US-08-391-340-6
/ Sequence 6, Application US/09391340A
/ Patent No. 6492211
/ GENERAL INFORMATION:
/ APPLICANT: Callen, Walter
/ APPLICANT: Mather, Eric
/ FILE REFERENCE: 09010/027001
/ TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF NOVEL POLYMERASES
/ CURRENT APPLICATION NUMBER: US/09/391,340A
/ EARLIER FILING DATE: 1999-09-07
/ EARLIER FILING DATE: 1997-08-06
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ LENGTH: 788
/ TYPE: PRT
/ ORGANISM: Archaeoglobus lithotrophicus
US-08-391-340-6

Query Match 37.34; Score 1563; DB 4; Length 788;
Best Local Similarity 41.34; Pred. No. 3.5e-135;
Matches 338; Conservative 154; Mismatches 273; Indels 54; Gaps 18;
Qy 1 MTEVTVFLDSYEVVGVKQFVINGIANGERNVILDSRFRFVALLAGAPQVQAQ 60
Db 1 MTKVGMGLADITENDRAVIRLAKCKDEG-IFTADHDSFQFYALKESGTFADIVK 59
Qy 61 -RIRALSRSPTGIVGDEKSKYFGSPREVLIRITVLPEAVREVLNVQDVELEA 119
Db 60 IKQVTKWTFP-LKVEETKATNGHEVFKVIRPQVFKLREVSQ---VLEIIRA 115
Qy 120 DIRAFKLLDHLDPFTFVTVKAEPLNAGFVQKVLVK--SRPELYGELAPTKL 177
Db 116 DIPFAKLLDNLKADMGVIGVVEREK-GLCYEKLIERDSQ-----F 163
Qy 178 POLRIALDPIEVSQSGSPREPDPVIVAKTDGDFVLFASGDKDQKPIREPVVK 237
Db 164 PELKAWDCEMSVQDPDQKPIVVISKGEYEL---NGNRELLRTPKAIIR 220

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QY 238 RYDDDIIVGNNHDPWYLLRRARILGILIMVTRVGAEPSTVGHVSVGRLNVLV 297
Db 231 DDDDDIIVGDSQDFWPTVKKWKKRAKAVLLGR--DRSELDGKGRPKIAKRLNVLV 278
QY 258 DYABENPEIKLSEVAVLYGKAGKSERVIMWMEIWDPOWDDPKPQLLOVADVRA 357
Db 279 DIAMSLDVKKVLEWVAFJG--KIEADIEANDIYHHTG--QDRSVIKYIKSDIHL 335
QY 358 TYGLAKLIPALQVSVGLPDQVGVGVLEPLVILIAFAPKELVAPNVERPET 417
Db 336 TYFABELPEVLEWLSMIRIFDVTYRSQGVQWELLSEARHGOELAPNPER-ADS 394
QY 418 GYLVVLEPGRHENTANDSKVPMWIKVNGPQVPLVROGKSGCGSEARVTH 477
Db 395 YEGAFVLEPAGLQVLEWILDFANFVSIETVSPPLVY--GRKDDCNV--APEVGH 450
QY 478 RRRSGDGFVYVLELRLKAGKMYKQKAGKYPGASRYVLEDRQKLUKULANSYGV 537
Db 451 KPNKQDFFERFLDMGIEKREKIKVMKVLKYSFYKLLDKATKVLNLSFGTGT 510
QY 538 NQKMGKQKQKAVNTAMHILITPAHIAKGLKIVGQTSLSVYVDERVEMFKI 597
Db 511 NLANWCKEAKNTANGRPFKTSNKLKGLVLEVYGTDS--FYVKKQSLSEAKE 570
QY 598 IK-----ELGFEIKLKVYKJLFFPKFAKRYKALLDGRDIDVGFANRQWELAK 650
Db 571 VAKLQKLEMPDQIDREYVETTFVE--KRYVAGLTQGRILVKGLEVRQWCELAK 629
QY 651 EYQTKVVEIKLSEVAVLYGKAGKSERVIMWMEIWDPOWDDPKPQLLOVADVRA 710
Db 630 KIQGVYHLLKSEKPRALRYKQVIEKAGTILIEDYVILNGLTRKSPKSNQV 689
QY 711 VAAMKMLSAQYVSGDKIVGVKGGKISORAMPYFVKD-----PSQIDV 758
Db 690 KAMKAKGKIVITGNGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 749
QY 759 TYVWHQIPAAALRILOFGLTEKKLKASATQKILPDF 797
Db 750 EYVYDQVLSVRLERFOTVBAQKAG--QTLNLF 787

RESULT 7
US-08-902-632-2
  1. Application US/0902632
  2. Patent No. 6008025
  3. GENERAL INFORMATION:
    1. APPLICANT: KOMATSUBARA, Hideyuki
    2. APPLICANT: KAWAMURA, Hiroyuki
    3. APPLICANT: KAWAMURA, Hiroyuki
    4. APPLICANT: KAWAMURA, Hiroyuki
    5. APPLICANT: KAWAMURA, Hiroyuki
    6. APPLICANT: TAGUCHI, Masahiro
    7. APPLICANT: TAGUCHI, Masahiro
  4. TITLE OF INVENTION: Modified Thermostable DNA Polymerase,
  5. TITLE OF INVENTION: Amplification
  6. ADDRESS: 1 Broadway
  7. CORRESPONDENCE ADDRESS:
  8. ADDRESSEE: Kenyon & Kenyon
  9. STREET: 1 Broadway
  10. CITY: New York
  11. STATE: NY
  12. COUNTRY: US
  13. ZIP: 10004
  14. COMPUTER READABLE FORM:
  15. MODUL TYPE: 3.50 inch floppy disk, 1.44 Mb storage
  16. MODUL TYPE: PC DOS/MS-DOS
  17. OPERATING SYSTEM: PC-DOS/MS-DOS
  18. SOFTWARE: WordPerfect 6.1 Windows
  19. CURRENT APPLICATION DATA:
  20. APPLICATION NUMBER: US/09/002/632
  21. FILING DATE: Concurrent Receipt

```

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 199911/96
FILING DATE: 30-JUL-1999
APPLICATION NUMBER: 30-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: GREGSON, Edward A.
REFERENCE/DOCKET NUMBER: 2418/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-425-7200
FAX: 212-425-7200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 amino acids
TYPE: amino acid
TILE: amino acid
MOLECULE TYPE: protein
US-08-902-632-2

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```

Query Match 29.5% Score 1237.5; Db 3; Length 774;
Best Local Similarity 36.6% Pred. No. 346-105;
Matches 303; Conservative 144; Mismatches 289; Indels 93; Gaps 22;

QY 8 VASGVSVKQKSPQVINGIANSRNVILIDRSFVFTALLAFAGADPKV---AQHIR 63
Db 2 TLUDYITDECFVIRFK--KENGSEKIEYDRFETFFVALLKQDSAEVSKVKTANGH 60
QY 64 ALSPKSPQIITDDEKQKFGKPRVLRKIVTPAEPVREIYVNGVQVDEVLDIRF 123
Db 61 TWVTVK---VEKQVKEGLRPVEMVKVLFTHQVPAIDKIKREKNAVITYEDVIFP 116
QY 124 AMRYLIDHDLFPFTWVFEABELENMGFRVDKVLVTSRSPFYSGALAPVTCPLRL 183
Db 117 AKYLLKNGLV-----PHSGD-----ELKGL 136
QY 184 ADIENVYSKQSPRPERDPIVIAVKTDDQVL-----FIASEKDKRKPFRFVEY 235
Db 139 ADIETLYHSEETAF--GFLIMISTADESGARVITKQVLDVFDVVSTRENGIKFLAV 192
QY 236 VAYDPIIDITVNNHFMPLVLLARALIGIKLDVTRVGAEPSTVGHG---VSVQRL 297
Db 198 VKEQDPVITVNDGNDFATYAKRCGLQKINFGALGD--GSEPKIQMDQFPAVEKGR 256
QY 293 NVQLYDAEMPEIKLSEVAVLYGKAGKSERVIMWMEIWDPOWDDPKPQLLOVAM 352
Db 287 FGLPVPVIRITPLVITLVAEYVPOQK--EKYTA--EITPAMETGENLEAVYSM 313
QY 353 DVDPATYGLAKLIPALQVSVGLPDQVGVGVLEPLVILIAFAPKELVAPNVER 412
Db 314 EDKAVTVEGLPELMEALQSLKIQSDMDVSSSTGNLVENFLEKAYERNELEAKD 373
QY 413 RPE-----ETFGALVLEPGRHENTANDSKVPMWIKVNGPQVPLVROGKSGC 467
Db 374 KEKALASRQVSEGVVPEPGRGEMVILIDRSFVFTALLAFAGADPKV---AQ 426
QY 468 GQV---ARSYKREKCPGKQFVITLLELRKGVREKWKVFPQSPVOLLDEROKA 524
Db 427 GQEVADVQVQGRFKCFQFTFSLGLDLERKOKIKAKKA--TIDPIERKLDDYKRA 485
QY 525 LKYLANSATQKMGSGAKGQKCAVNTAMHILITPAHIAKGLKIVGQTSLSVYDER 583
Db 486 IKLANSYGVGVYAGVABWTCQKSGVYANGREVTWTKIEBKYGKVLVSDTDQFP 545
QY 584 VTY-----DPEKVE---NFIKIKEL--GPHIKLEKVIETLFTBEAKRVAGLEGR 634
Db 546 ATIPGADGATVKKAMEFLYINAKLPALELVEYFQVYKFPV--TKKATVDEESKT 604
QY 635 IYGVFADGKELCALEQVTKVYVLTYSBVNKAVYKIVKELEBGKVPTEKLVNK 694
Db 605 TQGLIEVDRDWSHILNEZ--DQVYLDJADQVQVETAVLVEVYETLSKSTVFPPE 664

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QY 693 TLRKRLBTEAPHVAARMLSGVAVSRDQKIGVIVKQGRISQARMPYFVWDS 754
 DB 665 QITRLOQVATGVAVANLAAQVATGVAVISVILWGRSLDRAIP-FPEDFI 723
 QY 755 --QIDVTYVVDHQIIPAAIRILGVGTGTEKKASATQGTCTFFLAKK 801
 DB 724 KHYDASVLEIENQVAVENILDAAGTRKEDLRAVQKTRQVGLSMLKPK 772

RESULT 8

US-08-689-649-27

/ Sequence 37, Application US/08689649

/ Patent No. 5627116

/ GENERAL INFORMATION:

/ TITLE OF INVENTION: JOSEPH A. POL-II TYPE DNA

/ TITLE OF INVENTION: POLIMERASES

/ NUMBER OF SEQUENCES: 38

/ CORRESPONDENCE ADDRESS:

/ STREET: Suite 4700

/ CITY: Los Angeles

/ STATE: California

/ COUNTRY: U.S.A.

/ ZIP: 90071-2066

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

/ SOFTWARE: IBM PC compatible

/ OPERATING SYSTEM: IBM PC, DOS 5.0

/ SOFTWARE: Word Perfect 5.1

/ COUNTRY OF ORIGIN: USA

/ APPLICATION NUMBER: 08/689,649

/ FILING DATE: Filed Hereafter

/ CLASSIFICATION: 435

/ PRIORITY INFORMATION DATA:

/ APPLICATION DATA:

/ FILING DATE:

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Warburg, Richard J

/ ADDRESS: 220

/ REFERENCE/DOCKET NUMBER: 2,97

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (213) 489-1600

/ TELEFAX: (213) 955-0440

/ INFORMATION FOR SEQ ID NO: 37:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 776 amino acids

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULES TYPE: peptide

US-08-689-649-37

Query Match

Best Local Similarity 36.1%; Pred.No. 3.6e-105;

Matches 301; Conservative 154; Mismatches 283; Indels 95; Gaps 23;

QY 8 VLDSSTVSKPEQVILKGLANGERVLLDSSTVFTALLACDPOHY----AQIR 63

2 ILIDVDITSEKGVPTIRLFK--KNGVKFIEHDATFRVITALLADSDSKIEVKKITGEHG 60

QY 64 ALSRKPSTPLGVDEKQVGRVRLKIRITVLNVEVRELVNVDVLENDIRF 123

61 KTVR----IDVDEKVEKFLAKPTVWKLVLKHPQWPTITREKVAHPVDFIDP 116

QY 124 AMVLVDLIDLPFFFTVVAEPLKNGQFQVQVTVVSGPPELVGALATPKLPDL 183

117 ARKYLIDNGLI-----HWGGE-----BEKLI 138

QY 184 ADPIEVSKSGSPRPEDPVTIVANVDGSDVL-----FIAEGKDRKAPRIFVEY 235

DB 139 AFDELTVMHGE--EFGGRIIMISYDAENSAVITWQIDLPFVSVSRSEKMKFRLR 197
 QY 236 VGVSDRIIVGNVHSDHVPVLLQDRAITLQILGQVTRGVAFTTSMH---VSVGR 292
 DB 198 IREDDPILVITVNGDSFDPPLAKRAEKLQILQITGRD--GSEPGQRIQDVAWEKRL 256
 QY 293 NVLDVYAEWEPFIIKISLEVAEYLVQWKESEVYINMWEIDPMDPGPRLILQVAF 352
 DB 257 HFQIVTRITRITFTLEAVETAI--FGSPKRVAD--EIAWSESGENLERVAYSM 313
 QY 353 DYNVPLAKELKILFFQLGVYGLPQDGVQSGVGRLEWILIRAPQKCELVNREVS 412
 DB 314 EDNAVTELKSEFLMEIQLSLNQLPQDGVSVSSYGVNLTGVLAKANFENEVAFGS 373
 QY 413 RPE-----ETFGALVLEPLAGHENTALDPSFPMITKYNQDPTLVRPQKSGE 466
 DB 374 EEEVQRELSSTGQFVEFPEKAGMNTVLDPAFLPISLIITNVSFDLMALES---- 428
 QY 467 CCQWB--APVWEHFRFPCPFKTVLERLLEKRVBAMKVPDPSEYELLQKQAL 525
 DB 429 CNDYDVGQVGRCDIOPFPGALHGLLEKRLKIKTME--TQDPIKILLYDQKAI 487
 QY 526 KVLNAGSVQWGSQACVACRCBAVTAAGSHLRTA--INIAKGLKVLGYDQSPFV 547
 DB 488 KULANSFTGTGACAAHVCBAEVBTAAGSKYTELWKELEKPGFVLVITDQVIA 547
 QY 548 TYD-----PEKVENIKIIEELG--FTKLEKVKYLFTEAKRYVAGLSDGRIID 635
 DB 547 TIPOGSESHIKKALEFVYNSKLPGLLELEYEGFGKGFV--TKGVAVIDEGKVI 606
 QY 636 VQTEAVQWQDLNAGVQKVEVLTQSVKAVETKLVETSEKQVTEKLVHNT 695
 DB 607 RQLEIVRQDSEKATQARVLETILKGGVEBAVLEVIQVLANVETPEKLAITQ 666
 QY 696 LSGLEEVYTEAPVAAKMLSGVAVSRDQKIGVIVKQGRISQARMPYFVW-- 753
 DB 667 ITRLEHYKAIGHVAVAKLAAGVKTKGQWIGTVLRDQGTISNA---ILASEYD 723
 QY 754 S--QIDVTYVVDHQIIPAAIRILGVGTGTEKKASATQGTCTFFL-AKSK 803
 DB 724 KHYDASVLEIENQVAVENILDAAGTRKEDLRAVQKTRQVGLSMLKNSZ 776

RESULT 9

US-07-966-278-1

/ Sequence 1, Application US/07966278

/ Patent No. 7,518,252

/ GENERAL INFORMATION:

/ APPLICANT: Machur, Eric A

/ TITLE OF INVENTION: EXONUCLEASE-DEFICIENT THERMOSTABLE

/ TITLE OF INVENTION: PHOCOCUS FURTOSUS DNA POLYMERASE 1

/ NUMBER OF SEQUENCES:

/ CORRESPONDENCE ADDRESS:

/ ADDRESS: Thomas Fitting

/ STREET: 12526 High Bluff Road, Suite 300

/ CITY: San Diego

/ STATE: CA

/ COUNTRY: USA

/ ZIP: 92130

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: 3.5" Diskette

/ OPERATING SYSTEM: IBM PC compatible

/ SOFTWARE: PC-DOS/MS-DOS

/ COUNTRY OF ORIGIN: Patent Release #1.0, Version #1.25

/ APPLICATION NUMBER: US/07/966,278

/ FILING DATE: 1992/12/26

/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:

/ FILING DATE:

/ ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: STG0133P
 TELEPHONE: 619-792-3680
 TELEFAX: 619-792-8477
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 775 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FUNCTION: UNKNOWN
 ORGANISM: HUMAN
 ANTI-SENSE: NO
 US-07-966-278-1

Query Match 29.5%; Score 1236.5; DB 1; Length 775;
 Best Local Similarity 36.2%; Pred. No. 4 4e-105;
 Matches 301; Conservative 153; Mismatches 283; Indels 95; Gaps 23;

Qy 8 VLDSYEVGKEPQVINGAEKSERVILDSRFFITALLAPAGQPV---AQIR 63
 Db 2 LLVDVITTEGKVPILPK-KENKPKKEHRTNRYVIALSDSKIEVKKTGERS 60
 Qy 64 ALSPKPSIIIGDQMKQKPRFRVRLRTVLPENVRSELYVNOGVDEVLADRF 123
 Db 61 KLVK---LIVQVEKKFKLTKVWKLVEHQVPTIREKVRHNAVDFEIDPF 116
 Qy 124 ARVYLIDHLDLFFTFVVEAEPLNMGQFQVKNYVNSRPEPLVGSALPTKLPDLRI 183
 Db 117 AKVYLINGLI-----PDSG-----SEAL 138
 Qy 184 AFDLEYSKQSGFRPDPVIVAVTKDGDVL-----FIAGKDKRPFREFEV 235
 Db 139 AEDLVTHGE-EFGAGPILMISTADENKAVTWKIDLPVAVTSEREMKRFRI 197
 Qy 236 KRYDDPDIIVGNHHPHYLRARLIGIKLQVTRVCAEPTTSVGH---VSVGRL 292
 Db 198 IRKQDPIIVYTGQSPFPLKRAKAKGLTGID-GSEFPQKIDQWAVVNGRI 256
 Qy 293 NVLDVYAEAEPEKIKSLAEVAYGVWCKSERVINWDEIYDNDPKRFLQYAR 352
 Db 257 FHTVHTVITLHPTLVEAVEN--FGPKKQVAD--EAMANESGELKERVAKSV 313
 Qy 353 DVHRTYLAELKLPALQGLVGLDQVQNSVGRLEPWLTPAEPKMLVNVNR 412
 Db 314 EDKATYELGEKFLMEIQLRVGLQVQNSVSTGNVEMFLKAYENAVNPKS 373
 Qy 413 RPE-----STYGAIVLPIQVGHNTAVLDSESVYMIKVVQVQDPTLVREKCE 466
 Db 374 EEFYQRIARESTGQFVEKPEKSENVNVLDFALFSLITVHSPVTLBEG----- 428
 Qy 467 GCQCE-AREVKNRTPCPGFVLELRLAEKVRVAKWKPDPSPRYLLDSQAL 525
 Db 429 CNDYDAPVQGHGFKCIDFGFISLGHLEKQIKTMEKE--TQDPIKLIDRQAI 487
 Qy 526 KFAKNSITCVSGNSGKQVCAKAVNKHSLIETL-INIAKRLVNYTQDSFLV 584
 Db 488 KLANSTFGT-GAANARTCEKASVWAGKYLKELWKESEFQVLYIDTGLVA 547
 Qy 585 TVD-----PEKVENYTIKMEIG--FPIKLEKTYLFTFAKRYAGLLEGRIDI 635
 Db 548 TYPQSESKKALFEVYKLPOLLLELVEYTGTFQV--KSNVAVLDEBNKIT 606
 Qy 636 VQFPAVQDMLCAKEVQKTVKEIVLKTSEVNAIVPRTKVELEGKQVPEKLVNKT 695
 Db 607 RQLVYRDNSENGTQVAVETLNGVQDVENAVYFVYQLANVITPEKALTEQ 666
 Qy 686 LSKRLSEYETTEADPVAAKRLSAGVYSQDKGVIVNGGKRSQRAWPKV--DP 753
 Db 667 ITPLEHETKALGPHVAKQAMQVKKVFWGVIVGLVGGDQFSIRNA--LHAEHD 723
 Qy 754 S--QIDVTVYVHQIIPALALIGVGTETKELKASQKTLDFGL-AKKS 802

Db 724 KKKYDAVYTIENVLPVLRILGQYKREDYKQVKTQKVTGLTSMATKKS 775
 RESULT 10
 US-08-424-921-1
 ; Sequence 1, Application US/08424921
 ; Patent No. 5,515,522
 ; PERSAL INFORMATION:
 ; APPLICANT: Matour, Eric A
 ; TITLE OF INVENTION: PURIFIED THERMOSTABLE PYROCCUS
 ; TITLE OF INVENTION: PYROCCUS DNA POLYMERASE 1
 ; ADDRESS: 12256 High Bluff Road, Suite 300
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bingham & Fitting
 ; CITY: San Diego
 ; COUNTRY: USA
 ; ZIP: 92130
 ; COMPUTER READABLE FORM:
 ; FILE NAME: PEP1.DAT
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Recent Release #1.0, Version #1.25
 ; COMPILER: Microsoft C++ 4.0, 4.01, 4.02, 4.03
 ; APPLICATION NUMBER: US/08/424,921
 ; FILING DATE: 19-APR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA: US 07/803,627
 ; FILING DATE: 02-DEC-1991
 ; APPLICATION NUMBER: US 07/620,568
 ; FILING DATE: 03-DEC-1990
 ; PRIOR APPLICATION DATA: US 07/657,073
 ; FILING DATE: 19-FEB-1991
 ; PRIOR APPLICATION DATA: US 07/776,552
 ; FILING DATE: 03-DEC-1990
 ; NAME: Fitting, Thomas
 ; ATTORNEY/AGENT INFORMATION:
 ; REGISTRATION NUMBER: 34,163
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-792-3680
 ; TELEFAX: 619-792-8477
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 775 amino acids
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYDROTIC: NO
 ; ANTI-SENSE: NO
 ; US-08-424-921-1
 Query Match 29.5%; Score 1236.5; DB 1; Length 775;
 Best Local Similarity 36.2%; Pred. No. 4 4e-105;
 Matches 301; Conservative 153; Mismatches 283; Indels 95; Gaps 23;
 Qy 8 VLDSYEVGKEPQVINGAEKSERVILDSRFFITALLAPAGQPV---AQIR 63
 Db 2 LLVDVITTEGKVPILPK-KENKPKKEHRTNRYVIALSDSKIEVKKTGERS 60
 Qy 64 ALSPKPSIIIGDQMKQKPRFRVRLRTVLPENVRSELYVNOGVDEVLADRF 123
 Db 61 KLVK---LIVQVEKKFKLTKVWKLVEHQVPTIREKVRHNAVDFEIDPF 116
 Qy 124 ARVYLIDHLDLFFTFVVEAEPLNMGQFQVKNYVNSRPEPLVGSALPTKLPDLRI 183
 Db 117 AKVYLINGLI-----PDSG-----SEAL 138

```

Qy 184 AFDEIVTSKQSPREPDVPIVIAVTKDDQEVL-----FIAGKDKRPREFVEY 235
Db 139 ADPIETLHEGE-EPGQGTIMSTADQENKAVITKMDILVTVVSSERIMIRLEI 197
Qy 236 VKYVDPIIDVIGRRHEDPFLRLARILKGLDVTREVAEPPTSVGH- --VEVPRL 292
Db 198 IREKHDDPIIVTNDGSDPPFLAKRAEKGLKLTIGD--GSEPPQORIGDMTVAVGRI 256
Qy 293 NVDLVYDAEMPEIKSLSEVAVLAWKWSERVLNMMHEDVDPKPKLLQYAR 352
Db 257 HDPLVHVITINLFTPLLEAVYEA1-FQPKKEVAD--EIAKWSGEMSERVATSM 313
Qy 353 DVDRVATYGLAKILPALQGLSVTCPLDVLQVAGNSGRLEWYLITRAAKQMLNURVE 412
Db 314 EDMAKATYELGCEFFLEWELTGRVLQVPLMDVSRSTGSLVEMFLRAKAVENVAKPFS 373
Qy 413 REP-----ETFRALVLEPGRDHVHIAVDFSSMTKQVIMKYNVQDPLVRPEKOE 466
Db 374 EEEVQRLSESTVGVEPKPKOLMENVILDPALYSIIITHVGFOTLNLEG----- 428
Qy 467 CQWGE-ADVEVQRKRPQCPQFTYVRELEKSLVAKWPKYFDPSPVRLDRKQL 525
Db 428 QVNDYADQVGHKFKCDIPDITSLGHLLEKOKCKTQKE--TQDPEKTLDTQYAI 487
Qy 526 KLVANSQVAGKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 584
Db 488 KLVANSQVAGKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 547
Qy 585 TYD-----PKEVFIKITEELG--FEIKLEKYLKLEFFTEAKKQVAGLEQGRIDI 635
Db 548 TIPOGSEETKKALEFVYVINSKLPQULEVSEYFISQFV--TKKAVITDEBNAVIT 606
Qy 636 VQFNAVQDQCELAQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 695
Db 607 RQLEIVTQDQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 666
Qy 696 LSKLEEYTTQAPVAAKESAGVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 753
Db 667 ITPRARETQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 723
Qy 754 S-QIDVTVVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 802
Db 724 KUKYDASTYQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 775

RESULT 11
US-08-556-355A-1
Patent No. 5866395
GENERAL INFORMATION:
APPLICANT: MATHUR, Eric J.
TITLE OF INVENTION: Certified Thermostable Pyrococcus
METHOD OF INVENTION: Full Length DNA Polymerase I
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESS: Finnegan, Henderson, Farabow, Garrett &
ATTORNEY/AGENT INFORMATION:
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: SeqMan 4.0.5, SeqScribe 1.0, SeqScribe 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,355A
CLASSIFICATION: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/424,921

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FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,627
PUBLICATION DATE: 1995-05-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,846
FILING DATE: 21-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,073
FILING DATE: 19-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,568
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. Paul
REGISTRATION NUMBER: 32,013
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE LENGTH: 775 amino acids
TYPE: amino acid
STRANDNESS: single
MOLECULE TYPE: linear
MOLECULE TYPE: Protein
US-08-556-355A-1

Query Match
Similarity: 29.5%; Score 1236.5; DB 2; Length 775;
Matches 304; Conservative 153; Mismatches 283; Indels 95; Gaps 23;

Qy 8 VLDSEYVWKGQSPVINGIAENGERVVLDSRPTFFIALLAPADPKQV---AQRIE 63
Db 2 ILVDYITTEGKPIELF-KENSGKLENDITFFIALLDADSKLEVKKTGREG 60
Qy 64 ALSPKGFTIGVEDDKKTFGRPRVRLITVLEPAVREYELVNVQGVDEVLDIRP 123
Db 61 KLVN-----VDENKAPFQAPFTWKLLEHQDQFTTKEKPRHVAVDVETDIP 116
Qy 124 AMRVLLDHLQDFFVTFVVEAPELNGKGFVQVYLVKSRPEPLGALAPTKLPOLRI 183
Db 117 ACRLVDLGL-----PHGE-----SEKLI 138
Qy 184 AFDEIVTSKQSPREPDVPIVIAVTKDDQEVL-----FIAGKDKRPREFVEY 235
Db 139 ADPIETLHEGE-EPGQGTIMSTADQENKAVITKMDILVTVVSSERIMIRLEI 197
Qy 236 VKYVDPIIDVIGRRHEDPFLRLARILKGLDVTREVAEPPTSVGH- --VEVPRL 292
Db 198 IREKHDDPIIVTNDGSDPPFLAKRAEKGLKLTIGD--GSEPPQORIGDMTVAVGRI 256
Qy 293 NVDLVYDAEMPEIKSLSEVAVLAWKWSERVLNMMHEDVDPKPKLLQYAR 352
Db 257 HDPLVHVITINLFTPLLEAVYEA1-FQPKKEVAD--EIAKWSGEMSERVATSM 313
Qy 353 DVDRVATYGLAKILPALQGLSVTCPLDVLQVAGNSGRLEWYLITRAAKQMLNURVE 412
Db 314 EDMAKATYELGCEFFLEWELTGRVLQVPLMDVSRSTGSLVEMFLRAKAVENVAKPFS 373
Qy 413 REP-----ETFRALVLEPGRDHVHIAVDFSSMTKQVIMKYNVQDPLVRPEKOE 466
Db 374 EEEVQRLSESTVGVEPKPKOLMENVILDPALYSIIITHVGFOTLNLEG----- 428
Qy 467 CQWGE-ADVEVQRKRPQCPQFTYVRELEKSLVAKWPKYFDPSPVRLDRKQL 525
Db 428 QVNDYADQVGHKFKCDIPDITSLGHLLEKOKCKTQKE--TQDPEKTLDTQYAI 487
Qy 526 KLVANSQVAGKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 584
Db 488 KLVANSQVAGKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 547

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QY 585 TYD-----PEKVENFKIKIBELG--PEIKLKVYKRLFTPEKRYACGLDGRIDI 635
 Db 548 TIPOGSEBKEKALPEKVKYINIKLKPOLLELEYOTFGRGFFV-TKKRYAVINDSEKVIIT 606
 QY 636 VGFENVRGDCMLAKEQTKVYKIVLSEWKNVAYVTKVYKVELREGVYKPEIKVINTK 695
 Db 607 KGLTREDVSESTAKETQARVLETLTGHGDEVEAYVYKVELYOKLANYPYKPEIAIYEQ 666
 QY 696 LSKLEETITTEARHVAKMSAGYVSPCKYGVYKVGGRISORAWPYKVK--DP 753
 Db 667 ITRPELHEVIAKPRHVAKLANGVKIKPVGIVTILGSDGPGISNRA--ILAEYDP 723
 QY 754 S--QIDVTYVGHQIIPALRLIGVTEKLVKASRQKLEDFI-AKXS 802
 Db 724 KKKYDASVYIENQVLEAVLALLEGYKRYEDYKRYKTRAGVLTSLNTKAS 775

RESULT 12

US-07-803-627A-1
 ; Sequence 1, Application US/07803627A
 ; General Information:
 ; APPLICANT: MATHUR, Eric J.
 ; TITLE OF INVENTION: Purified Thermostable Pyrococcus
 ; TITLE OF INVENTION: furiosus DNA Polymerase I
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEES: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESS: Dunner, L.L.P.
 ; STREET: 1300 I Street, N.W.
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005

COCKER, J. H. 1999. A
 ; MEDIAN TYPE. EMBL
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CUI: 1999-01-01
 ; APPLICATION NUMBER: US/07/803,627A
 ; FILING DATE: 02-DEC-1991
 ; CLASSIFICATION: 435
 ; PRIORITY NUMBER: US 07/776,552
 ; FILING DATE: 14-OCT-1991
 ; PRIOR APPLICATION DATA:
 ; PRIORITY NUMBER: US 07/657,073
 ; FILING DATE: 02-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/620,568
 ; FILING DATE: 03-DEC-1990
 ; ATTORNEY: Barker, M. Paul
 ; REGISTRATION NUMBER: 32,013
 ; REFERENCE/DOCKET NUMBER: 04121.0004-00
 ; TECHNICAL INFORMATION:
 ; TELEPHONE: (202)408-4400
 ; TELEFAX: (202)408-4400
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-803-627A-1

Query Match 29.5%; Score 1236.5; DB 2; Length 775;
 Best Local Similarity 36.2%; Pred. No. 4.4e-105;
 Matches 301; Conservative 153; Mismatches 283; Indels 95; Gaps 23;
 QY 8 VLDSSVEYVKEPVLINGIAENGSRVRLIDRSFPETVALLAGADPKQV---AQRIR 63

Db 2 ILDDVITEKEKQVIRLFK-KKNGKFKIEHDFPTPTVALLADSSKEVVKITGSHG 60
 QY 64 ALASFPKPTIGIOWDKKKYKGGPRVRLVIAVYVAVREYVETLVNVOVDVLEADIR 123
 Db 61 KIVA-----LVQVKKPKLGEPTVILKQVLEKPVITKEVNEVHPAVDITDIP 116
 QY 124 AKVILDHQILPTVTVVREAPLEPKNGQFVQKIVLVSRPEFLVGSALPAKTAQPOLIIL 183
 Db 117 AKVILDKGL-----PKGSE-----REKIL 138
 QY 184 ADPIEVYSKQSGSRPEPDVIVIAKVTDDDEVL-----FIAGKDDKPKIRFVEY 235
 Db 139 ADPIEVYVREGE-EPGQGPILVSVADNENKLTWNKIDLPYEVVSSEKRLKAPRI 197
 QY 236 VYVDDPIIVQVNNHEDHPTLLRGARLIGKIDVTRVGAEPITSVGHG---VSVPEQL 292
 Db 198 INEKPDIIVTTHNGSDPFLAKSEALQILKLTIGD-GSEPKQKIGDMTAVEVKRI 256
 QY 293 NVYDVAEMPEIKISLEEVARYLVGKMSERVINWMEI PDYMDPKRPLALQYAR 352
 Db 257 HGVITVTRITLQVLTLEAVTAJ-PQPKRYVAD--ELAKMEGSELENVAKYV 313
 QY 353 DDVATVYGLAKLIFALQVLTGVLDDQVGVGAFLEWLTIAAFKMKELVNVKE 412
 Db 314 EDKATVYELKEFLMEIQLSKVLQGVADVRSSTGMLVEMFLRLKATREVAENAFNS 373
 QY 413 REP-----ETVSGAVLEPLUGVHENTVADLSSNWMYKINXGPTLVREGEKGE 466
 Db 374 BEFYRLRESEVYTGCFVAFSEKGLMENVLQDFALPFIITNHSPTPLMSEG---- 428
 QY 467 GCGWE-APFVSEHPECPGCFKTVLELLSLKRVSRKSKVYFDSPEVLLDSEKAL 525
 Db 429 CNDYDIAQVGHFQCFI-PGFTPELGLHLLERKIKITQMS-TQPIEKILLDVKQAI 487
 QY 526 KULANSYVQWGRGKRYCGRKAMVYANGSHLITFA-INYARKLVGYGTOSLPV 584
 Db 488 KULANSFYGTGNARMYCKEASVTANGKAYTELWHELEERKGFVXIIDGVLA 547
 QY 585 TYD-----PEKVENFKIKIBELG--PEIKLKVYKRLFTPEKRYACGLDGRIDI 635
 Db 548 TIPOGSEBKEKALPEKVKYINIKLKPOLLELEYOTFGRGFFV-TKKRYAVINDSEKVIIT 606
 QY 636 VGFENVRGDCMLAKEQTKVYKIVLSEWKNVAYVTKVYKVELREGVYKPEIKVINTK 695
 Db 607 KGLTREDVSESTAKETQARVLETLTGHGDEVEAYVYKVELYOKLANYPYKPEIAIYEQ 666
 QY 696 LSKLEETITTEARHVAKMSAGYVSPCKYGVYKVGGRISORAWPYKVK--DP 753
 Db 667 ITRPELHEVIAKPRHVAKLANGVKIKPVGIVTILGSDGPGISNRA--ILAEYDP 723
 QY 754 S--QIDVTYVGHQIIPALRLIGVTEKLVKASRQKLEDFI-PDEL-AKXS 802
 Db 724 KKKYDASVYIENQVLEAVLALLEGYKRYEDYKRYKTRAGVLTSLNTKAS 775

RESULT 13

US-07-803-627A-1
 ; Sequence 1, Application US/09244899A
 ; Patent No. 6489150
 ; GENERAL INFORMATION:
 ; APPLICANT: MATHUR, Eric J.
 ; TITLE OF INVENTION: Purified Thermostable Pyrococcus
 ; TITLE OF INVENTION: furiosus DNA Polymerase I
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEES: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESS: Dunner, L.L.P.
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005

```

COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: PC-DOS/MS-DOS, Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/244, 849A
FILING DATE:
PRIORITY DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/135, 064
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603, 627
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/776, 552
FILING DATE: 19-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620, 568
FILING DATE: 03-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. Paul, 32, 013
TELEPHONE: 502/408-0000
REFERENCE/DOCKET NUMBER: 04121.0004-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 502/408-0000
FAX: 502/408-0000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 775 amino acids
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-244-849A-1

Query Match
Best Local Similarity 36.24; Pred. No. 4,4e-105;
Matches 301; Conservative 153; Mismatches 283; Indels 95; Gaps 23;

Qy 8 VLDSVSGVPEVINGLANSERVVLDISFRFVALLAGAPKGV---AQR 63
Db 2 ILVDVITKCPKPVILKFK-KNKKQFIMKHQRTFFPIALLRDSKIEKVIK 60
Qy 64 ALSRKSPEIIVEDKQKSPKRVKIRTVLPAVRELVKVDVGVLEADIRP 123
Db 6 KIVR---LVDEKVKFALGRPTVWKVLYLEHPQVPTTKVSRHVAVDIFDIFP 116
Qy 124 AKVYLIDHLPFTVWAVEALEPNQGFVDKVLVSRPEYGLCALAPTKLPDLRIL 183
Db 117 AKVYLIDHLPFTVWAVEALEPNQGFVDKVLVSRPEYGLCALAPTKLPDLRIL 138
Qy 184 APDIEWKSGSPKSPRPVIVAKVDQEVL-----FVAGSDKRPKEVEY 235
Db 139 APDITETHEGE-SFKGQFIMISYADNKAIVTQDLPVVEVSSRHEMKRFLRI 197
Qy 236 VKYDQVITVNNHNFQVPLPRLKTLVDVTVGSGEPTTSVGH---VSVQRL 292
Db 198 IRKQDQDILVTVNDGSPDFPLAKAEGKGLTKTGQD-GSEPPQKQIGMTAVKRI 256
Qy 293 NVYLDVYAEEMPKIKSLSEKLVKGVKSEVILVWNGEIVDQVDDPKVPLLQVAV 352
Db 297 HPDVTITVITVPLVTLVAVTAL-FGPKPKVYAD--ELAKMGSGLNLERVATKM 313
Qy 353 DVWRTATGLKPLKPLATSVYGLPDLQNCAGVRLKVEKPLKIDPAKQKELVNVSE 412
Db 314 EDAAKATLGKPEFMETQLSRLVQVQIMVDSSTGNCVEMFLKAVERNVAPKPS 373
Qy 413 RPE-----ETFGVAVLEPLGCVHNVNIAVDTSNTPIMKIVGPDPLVREKCE 466

374 EREYQRELESTYGGVPEKGLMENVLVDLFRALVPSLITTHNSVPTUNLEG-----428
467 CCQCE-APRVNHFRCPPFFVLELLELRVRAEMKPPSPFVILLERQKAL 525
429 QNYADPAGVGHFCKPSTPSELLQHLLEKIKNTKME-CQPIKILLYVQKAL 487
526 KVLAASTGVGHSNANTCRCKAVTNGRHLRTA-IMIAKGLKLVYGTDTSLFV 584
488 KLLANSPVTVGVANVAVTCKGASVYKMSKYLIVWNSLEKGFNVLYDGLVA 547
585 TYD-----PEKVENTKIKKEELG--FKILEKVKTELEFFTKAKYAGLEORIDI 635
548 TIPGSESEIKGLLEKLVNYSKGLLELEVDFHGGFV-TKRYAVIDEGKIT 606
636 VGFVAVRGWCELANEYQVKEVLTSTNNVAVETVLEKEEKVPTEKLYIMKT 695
607 RGLLEVRUNSELINEQVRYLETLIAGDGEENRVLEVIOKANTLEIPPELLATFQ 666
696 LSKLELEYTTHAVVAAKSLGAGVRSYKGIQVIVKGGRIQSGAMPVFWK--DP 753
667 ITRPLEYKAGHVAVYKGLAKGVKQKRWIGIVLVRGDDPISNR-----ILANSTDP 723
754 S-QIDVTYVVDWQIIPALRLIGVLTETKSKASATQNTKFDPL-AKGS 802
724 KKHGTDAHYTHQVLAIVLISGFVRYKRELYKQTRVGLTSMVAKKS 775

RESULT 14
US-09-073-354-1 Application US/09073354
Patent No. 6033859
GENERAL INFORMATION:
APPLICANT: KITABAYASHI, Masao
INVENTOR: KAWAMURA, Yoshitaka
APPLICANT: INOUE, Hiroaki
APPLICANT: KAWAMURA, Bunsel
APPLICANT: KAWAMURA, Yoshitaka
APPLICANT: KAWAMURA, Bunsel
APPLICANT: TANIGUCHI, Masahiro
APPLICANT: MORIKAWA, Masaaki
TITLE OF INVENTION: A thermostable DNA polymerase and kits for
amplifying nucleic acids
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Kenyon & Kenyon
CITY: Washington
STATE: D.C.
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: PC-DOS/MS-DOS, Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/073, 354
FILING DATE: Concurrent herewith
PRIORITY DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/656, 005
FILING DATE: 24 MAY 1996
FILING DATE: 31 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 1:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 774 amino acids
TYPE: amino acid
STRANDNESS: double
TOPOLOGY: linear
WORD: 1000
US-09-073-354-1

Query Match 29.5%; Score 1234.5; DB 3; Length 774;

Best Local Similarity 36.4%; Red. No. 686; 95;
Matches 307; Conservative 145; Mismatches 289; Indels 93; Gaps 22;

Qy	8	VDSSTVEVKEQPTVIMGAIAGNRRGVLDISFPIFFALLAPQDPVY	---	Qy	63	ADIR 63
Db	2	LDVDTTDEGQVTRIFK-KENGEKLEYDFTFFALLDQSAIEVVKTKTSHG	60	Db	2	LDVDTTDEGQVTRIFK-KENGEKLEYDFTFFALLDQSAIEVVKTKTSHG 60
Qy	64	ALSPKSPFISGVDDKQKATFGSPRVLYRITVLPANREVLNVNVDGVLEADIRE	123	Qy	64	ALSPKSPFISGVDDKQKATFGSPRVLYRITVLPANREVLNVNVDGVLEADIRE 123
Db	61	TVYVYR-----VEKQKFLGHPVEVWKLFTFHQVPAIRKDEHGNVLDITDIFP	116	Db	61	TVYVYR-----VEKQKFLGHPVEVWKLFTFHQVPAIRKDEHGNVLDITDIFP 116
Qy	117	ACRYLLDGLV-----PMED-----ELMG 138		Qy	124	ARYLLDHLDPFTTVEAREPLENGFVYKLVKSRPEELVGLGALAPTKLPDLAIL 183
Db	117	ACRYLLDGLV-----PMED-----ELMG 138		Db	117	ACRYLLDGLV-----PMED-----ELMG 138
Qy	184	ADTVLVSQKSPREPDPIVAVTKDDGDLV-----FIAGQDKRPFREFVEY	235	Qy	184	ADTVLVSQKSPREPDPIVAVTKDDGDLV-----FIAGQDKRPFREFVEY 235
Db	139	ADPTQVTHEGEFSAF-GPILMIYADEAGAVITKQVDPVYVTVSTREMIKFLRV	197	Db	139	ADPTQVTHEGEFSAF-GPILMIYADEAGAVITKQVDPVYVTVSTREMIKFLRV 197
Qy	236	KQVYDPDITVGNVNNHDPVLRARLIGLDITRVRGAEFTVSVGH-----VSVPGL	292	Qy	236	KQVYDPDITVGNVNNHDPVLRARLIGLDITRVRGAEFTVSVGH-----VSVPGL 292
Db	198	VKEQDVPDLITTINGDNPFAIKKCKELGINFALGD--GESEKIQMDRFAVEVKRI	256	Db	198	VKEQDVPDLITTINGDNPFAIKKCKELGINFALGD--GESEKIQMDRFAVEVKRI 256
Qy	293	NVDLYVAEMPEIKLISIEVAVLYGVKSKSRVINNWEIPDYDDKRPALLQYAR	352	Qy	293	NVDLYVAEMPEIKLISIEVAVLYGVKSKSRVINNWEIPDYDDKRPALLQYAR 352
Db	257	HFDTYVTRITMLPTVLEAVNAVFGQPK-EKYVAE--BITPANTGTENLERYAKEM	313	Db	257	HFDTYVTRITMLPTVLEAVNAVFGQPK-EKYVAE--BITPANTGTENLERYAKEM 313
Qy	353	DIVRATGLAKLTPALQVATVQLPQVQVNSVGELEKWLITRABVOKELVNVRE	412	Qy	353	DIVRATGLAKLTPALQVATVQLPQVQVNSVGELEKWLITRABVOKELVNVRE 412
Db	314	EDAKVTELGEEFLHQAQSLR-LQSLMVDSRSTGNLWELFLKAVENELANPFO	373	Db	314	EDAKVTELGEEFLHQAQSLR-LQSLMVDSRSTGNLWELFLKAVENELANPFO 373
Qy	413	REP-----ETRQGLVLESGVHNIAVDSQSMYNTKYNQDPTVRRGKCEC	467	Qy	413	REP-----ETRQGLVLESGVHNIAVDSQSMYNTKYNQDPTVRRGKCEC 467
Db	374	EKEALRSGYEGQVKEPGEGLWENIVLDFELPSHIIITNNVSPDTLME-----	426	Db	374	EKEALRSGYEGQVKEPGEGLWENIVLDFELPSHIIITNNVSPDTLME----- 426
Qy	428	GCWE--APETVGRFRCQPTVYKVLKELLKRVAAKAKYPPSPFVKLLQVKA	524	Qy	428	GCWE--APETVGRFRCQPTVYKVLKELLKRVAAKAKYPPSPFVKLLQVKA 524
Db	467	GVYVAVQVQVQKQKQFPPTSLQDLDEQKIKKOKA-TIDPLEKLLVQGA	485	Db	467	GVYVAVQVQVQKQKQFPPTSLQDLDEQKIKKOKA-TIDPLEKLLVQGA 485
Qy	525	LKVLNANVQVQVQKQKQFPPTSLQDLDEQKIKKOKA-TIDPLEKLLVQGA	583	Qy	525	LKVLNANVQVQVQKQKQFPPTSLQDLDEQKIKKOKA-TIDPLEKLLVQGA 583
Db	486	IKLANSIYQVQVQKQKQFPPTSLQDLDEQKIKKOKA-TIDPLEKLLVQGA	545	Db	486	IKLANSIYQVQVQKQKQFPPTSLQDLDEQKIKKOKA-TIDPLEKLLVQGA 545
Qy	584	VTY--DRENE-----NPKIKTEL--GEFLKEVATGTFPTAKKAYAGLEPDRD	634	Qy	584	VTY--DRENE-----NPKIKTEL--GEFLKEVATGTFPTAKKAYAGLEPDRD 634
Db	546	ATFDQADAKVKKANFETITNKLQVGLNGLNGLNGLNGLNGLNGLNGLNGLNGLN	604	Db	546	ATFDQADAKVKKANFETITNKLQVGLNGLNGLNGLNGLNGLNGLNGLNGLNGLN 604
Qy	635	IVGEVAREGMCLEKQVTVLVIKTSKAVKAVKAVKAVKAVKAVKAVKAVKAVKAV	694	Qy	635	IVGEVAREGMCLEKQVTVLVIKTSKAVKAVKAVKAVKAVKAVKAVKAVKAVKAV 694
Db	605	TRGELTVRRQSEIATQVATQVLEALQVLEALQVLEALQVLEALQVLEALQVLEAL	664	Db	605	TRGELTVRRQSEIATQVATQVLEALQVLEALQVLEALQVLEALQVLEALQVLEAL 664
Qy	695	TLSNLEETITAPVAVAKMAGVYVSGDKIGVIVMGQGGISQVAPVNDVDS	754	Qy	695	TLSNLEETITAPVAVAKMAGVYVSGDKIGVIVMGQGGISQVAPVNDVDS 754
Db	665	QITRDLDTATQVGHVAVLAANGVIRKGVISVYLSKSGRIQDAPL-FREDFP	723	Db	665	QITRDLDTATQVGHVAVLAANGVIRKGVISVYLSKSGRIQDAPL-FREDFP 723
Qy	755	--ODIVTYVDRQLIPALRLIGVYGTGTEKLKASATQNTQVFLAKK	801	Qy	755	--ODIVTYVDRQLIPALRLIGVYGTGTEKLKASATQNTQVFLAKK 801
Db	724	KHKYDAETIENQVAVFVRLQVATVREEDLYVQNTQVGLSMVLEKPK	772	Db	724	KHKYDAETIENQVAVFVRLQVATVREEDLYVQNTQVGLSMVLEKPK 772

RESULT 15

US-08-655-005A-1

; Sequence 1, Application US/0865005A

; Patent No. 6054301

GENERAL INFORMATION:
APPLICANT: KITABAYASHI, Masao
APPLICANT: ARAKAWA, Taku
APPLICANT: INOUE, Hiroaki
APPLICANT: KAWABE, Toshiaki
APPLICANT: KAWABE, Toshihisa
APPLICANT: KAWABE, Toshiaki
APPLICANT: IMANAGA, Tadayuki
APPLICANT: TAKAGI, Masahiro
APPLICANT: TAKAGI, Masahiro
APPLICANT: TAKAGI, Masahiro
TITLE OF INVENTION: A Method of Amplifying Nucleic
MATERIALS OF INVENTION: Acid and A Reagent Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" floppy disk
CHARACTER SET: ASCII
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656, 005A
CLASSIFICATION: 435
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 134096/95
FILING DATE: 31 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2418/3
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 amino acids
TYPE: amino acid
STRANDNESS: double
TOPOLOGY: linear
WORD: 1000
US-08-655-005A-1

Query Match 29.5%; Score 1234.5; DB 3; Length 774;
Best Local Similarity 36.4%; Red. No. 686; 95;
Matches 307; Conservative 145; Mismatches 289; Indels 93; Gaps 22;

Qy	6	VDSSTVEVKEQPTVIMGAIAGNRRGVLDISFPIFFALLAPQDPVY	---	Qy	63	ADIR 63
Db	2	LDVDTTDEGQVTRIFK-KENGEKLEYDFTFFALLDQSAIEVVKTKTSHG	60	Db	2	LDVDTTDEGQVTRIFK-KENGEKLEYDFTFFALLDQSAIEVVKTKTSHG 60
Qy	64	ALSPKSPFISGVDDKQKATFGSPRVLYRITVLPANREVLNVNVDGVLEADIRE	123	Qy	64	ALSPKSPFISGVDDKQKATFGSPRVLYRITVLPANREVLNVNVDGVLEADIRE 123
Db	61	TVYVYR-----VEKQKFLGHPVEVWKLFTFHQVPAIRKDEHGNVLDITDIFP	116	Db	61	TVYVYR-----VEKQKFLGHPVEVWKLFTFHQVPAIRKDEHGNVLDITDIFP 116
Qy	117	ACRYLLDGLV-----PMED-----ELMG 138		Qy	124	ARYLLDHLDPFTTVEAREPLENGFVYKLVKSRPEELVGLGALAPTKLPDLAIL 183
Db	117	ACRYLLDGLV-----PMED-----ELMG 138		Db	117	ACRYLLDGLV-----PMED-----ELMG 138
Qy	184	ADTVLVSQKSPREPDPIVAVTKDDGDLV-----FIAGQDKRPFREFVEY	235	Qy	184	ADTVLVSQKSPREPDPIVAVTKDDGDLV-----FIAGQDKRPFREFVEY 235
Db	139	ADPTQVTHEGEFSAF-GPILMIYADEAGAVITKQVDPVYVTVSTREMIKFLRV	197	Db	139	ADPTQVTHEGEFSAF-GPILMIYADEAGAVITKQVDPVYVTVSTREMIKFLRV 197
Qy	236	KQVYDPDITVGNVNNHDPVLRARLIGLDITRVRGAEFTVSVGH-----VSVPGL	292	Qy	236	KQVYDPDITVGNVNNHDPVLRARLIGLDITRVRGAEFTVSVGH-----VSVPGL 292
Db	198	VKEQDVPDLITTINGDNPFAIKKCKELGINFALGD--GESEKIQMDRFAVEVKRI	256	Db	198	VKEQDVPDLITTINGDNPFAIKKCKELGINFALGD--GESEKIQMDRFAVEVKRI 256
Qy	293	NVDLYVAEMPEIKLISIEVAVLYGVKSKSRVINNWEIPDYDDKRPALLQYAR	352	Qy	293	NVDLYVAEMPEIKLISIEVAVLYGVKSKSRVINNWEIPDYDDKRPALLQYAR 352

Db 257 HPLVFIERTINLEPTLBAVAVFGQK-EKYAL--BITPAMETOENLERNVARYSM 313
 QY 353 DOVRATYGLAEKLPFAIQSLVYVGLDQDGMSTVGFLENVILBAKPKKELVPRVYE 412
 Db 314 EDKAVTYELGEFLPMEAGLSRLQGLSDMVSSESTONLVEHFLKRAYERNELAPKPD 373
 QY 413 RBE---ETTRGATVLEPLRGVHENVIAVLDPSSMYPNIMIXYNGPDTLVRECKGBC 467
 Db 374 EKSLARRQSGEGYKVEPFGLENIVLDFRSLYFSIIITHNVSPDTLRE----- 426
 QY 468 GQWE---APEYGBRRCPCGFPKTVLLELELEVRABMKYPPSPRYELLDESOKA 524
 Db 427 GCKSYDPAQVQGRFCDFGFI9SLGDLLEKQIKKOKA-TIDPIERKLLDYROA 485
 QY 525 LKVLNASTYGMWGSABWYCEOKAVTANGSHLFTAI-NIARLGLKAVYIGDTSLF 583
 Db 486 IKILANSTYGYVIAARWYCEOKAVTANGSEYITIMIKIEKYGFKVITSIDTOFF 545
 QY 584 VTY--DPEKYE---NFIKILKEEL--GFEIGLEKYKELFTEAKRYAGLLEDGTD 634
 Db 546 ATIFGADATYKQAMEFLANVINKLPDALSVEYGFYAGFFV-TNCKXAVDEBKIT 604
 QY 635 IVGPENAVGDCSLAKVCTQVTVLUTSBNVAVYVYKIVKVELEKQVTEKLVNK 694
 Db 605 TGLGLEIYAEEDMSIAKSTAOARVLBALLAGDVEKAVHVKSEVTEKLSKYVPPKLVHE 664
 QY 695 TLAKGLSEYFTEARNVAAKMGAGYRUSPCKTGVYUUKGCGRISORANRYFWKQDS 754
 Db 665 QITRDLKDYKATCHVAVAKKLAARQVKIRGTVISIVILKSGRIGORAI-PFDEPFT 723
 QY 755 --QIUVTVYVDRHIIIPALAILGYGCTEKKKASATQKMLFDPLAKX 801
 Db 724 KXKTDASYIENNVLEVERILANFYREDLAKYKTRQVGLSAMLKPK 772

Search completed: November 25, 2003, 15:00:59
 Job time : 25 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 12:04:39 ; Search time 0756 Seconds
11308.047 Million cell updates/sec

Title: US-10-034-849-1

Filter: score: 1 tagctgaagtcgtcttcc.....tagccaagaagcagctaa 2412

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 288071 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:

1: gb:htg.*

2: gb:htg.*

3: gb:htg.*

4: gb:htg.*

5: gb:htg.*

6: gb:htg.*

7: gb:htg.*

8: gb:htg.*

9: gb:htg.*

10: gb:htg.*

11: gb:htg.*

12: gb:htg.*

13: gb:htg.*

14: gb:htg.*

15: gb:htg.*

16: gb:htg.*

17: gb:htg.*

18: gb:htg.*

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21: gb:htg.*

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40: gb:htg.*

41: gb:htg.*

42: gb:htg.*

43: gb:htg.*

44: gb:htg.*

45: gb:htg.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2412	100.0	2412	6	AB072898	Sequence
2	2412	100.0	2412	6	AB072898	Sequence
3	2412	100.0	2412	6	AA669431	Sequence
4	2412	100.0	2412	6	AB060287	Isolation
5	2412	100.0	2412	6	AB060287	Isolation
6	1071.2	44.4	3068	6	E19436	Sequence
7	1071.2	44.4	3069	1	E19436	Sequence
8	1069.6	44.4	2430	6	E19436	Sequence
9	1069.6	44.4	2430	6	E19436	Sequence
10	1069.6	44.4	2430	6	E19436	Sequence
11	735.2	30.5	2319	1	AB017501	Aeropryum
12	735.2	30.5	2319	6	E36726	Novel DNA p
13	580	24.0	2610	6	AB032158	Sequence
14	580	24.0	2610	6	AB032158	Sequence
15	574.6	23.8	266050	1	AP000988	Salicob
16	570	23.6	10560	1	AE009857	Probacul
17	569.8	23.6	2346	1	AB032376	Sulfurip
18	276	11.6	2371	1	AB010700	Archaeogl
19	276	11.6	2371	1	AB010700	Archaeogl
20	279	11.6	2367	6	AA669433	Sequence
21	279	11.6	2367	6	BD080288	Isolation
22	204.2	8.5	2376	6	E13954	Artificial
23	191.4	7.9	2325	6	E15069	gDNA encodi
24	191.4	7.9	2325	6	E15069	gDNA encodi
25	191.4	7.9	2325	6	E15069	gDNA encodi
26	191.4	7.9	2325	6	E15069	gDNA encodi
27	189.6	7.9	2325	6	E15069	gDNA encodi
28	189.6	7.9	2325	6	E15069	gDNA encodi
29	184.8	7.7	2335	6	BD078736	Sequence
30	177.4	7.4	2322	6	AA113132	Sequence
31	174.8	7.2	2331	6	AA135456	Sequence
32	174.8	7.2	2331	6	AA135456	Sequence
33	174.4	7.2	2374	6	E14137	DNA encodin
34	173	7.2	2840	1	SS092874	Salicob
35	167.2	6.9	26118	1	CNSPAX06	Pyrococcu
36	167.2	6.9	26118	1	CNSPAX06	Pyrococcu
37	165.4	6.8	2995	1	PANAPOL	Sequence
38	163.2	6.8	2322	6	A79152	Sequence
39	163.2	6.8	2322	6	BD009950	Thermota
40	162.6	6.7	4446	6	PS0710POL	Pyrococcu
41	162.6	6.7	4446	6	PS0710POL	Pyrococcu
42	162.2	6.7	2995	6	AE68744	Sequence 2
43	157.4	6.5	2408	1	TS047108	Pyrococcu
44	150.8	6.3	2391	1	PS025032	Pyrococcu
45	146.2	6.1	2734	6	E13626	Sequence 13

ALIGNMENTS

RESULT 1

LOCUS

AB072898

Accession

AB072898

Accession

AB072898.1

Keywords

Unknown.

Source

Unclassified.

Organism

1 (bases 1 to 2412)

Reference

Cullen W. and Matur E.J.

Isolation and identification of polymerases

Patent: US 5948666, 1999,

Location/Qualifiers

2412 bp DNA

linear

PAT 28-AUG-2000

3 from patent US 5948666.

AB072898.1

GI:9999661

Unknown.

Unclassified.

1 (bases 1 to 2412)

Reference

Cullen W. and Matur E.J.

Isolation and identification of polymerases

Patent: US 5948666, 1999,

Location/Qualifiers

Pred. No. is the number of residues predicted by chance to have a

source	1..-2412 /organism: 'unknown'	BASE COUNT 631 a 512 c 707 g	562 t
Query Match	100.0%; Score 2412; DB 6; Length 2412;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 2412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 ATGACTGAGTCTGATTCACGGTTTATGACTTACAGCTAGAGGCTTGTGTAAGAGCT 60		961 ATGAGAGAGTGAAGCGTTATCATCATGTTGTGGAGATTCCAGACTATTGGAGAC 1020
Db	1 ATGACTGAGTCTGATTCACGGTTTATGACTTACAGCTAGAGGCTTGTGTAAGAGCT 60		961 ATGAGAGAGTGAAGCGTTATCATCATGTTGTGGAGATTCCAGACTATTGGAGAC 1020
Qy	61 CAGGAGATGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120		1021 CGAAGAGAGACATTAATTAAGTCAATATGACGAGAGAGAGAGAGAGAGAGAGAG 1080
Db	61 CAGGAGATGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120		1021 CGAAGAGAGACATTAATTAAGTCAATATGACGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy	121 TTGCGGCTGATCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180		1081 TTGAGCGAGAGAGATTAATTCAGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db	121 TTGCGGCTGATCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180		1081 TTGAGCGAGAGAGATTAATTCAGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy	181 CATTATGATGATGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240		1141 GACGAGATGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db	181 CATTATGATGATGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240		1141 GACGAGATGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Qy	241 ATGACTTCTGAGGCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300		1201 TTGAGCGAGAGAGCTGTGCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db	241 ATGACTTCTGAGGCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300		1201 TTGAGCGAGAGAGCTGTGCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Qy	301 AGGAGATGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360		1261 GCTATGATCTTGAAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db	301 AGGAGATGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360		1261 GCTATGATCTTGAAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Qy	361 ATAGGCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420		1321 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db	361 ATAGGCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420		1321 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Qy	421 ATAGGCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480		1381 GGTGAG 1440
Db	421 ATAGGCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480		1381 GGTGAG 1440
Qy	481 ATAGGCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540		1441 AGGTGCTGCTGCGGCTTCTTCAAGACAGTCTTGAAGAGCTTGTAGAGCTTGTAAAGGCT 1500
Db	481 ATAGGCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540		1441 AGGTGCTGCTGCGGCTTCTTCAAGACAGTCTTGAAGAGCTTGTAGAGCTTGTAAAGGCT 1500
Qy	541 AGGATGCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600		1501 GTGCTGCTGAAATGAGAGAGATCTCTCGATAGCCAGAGATATCGACTTGTGATGAA 1560
Db	541 AGGATGCTGATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600		1501 GTGCTGCTGAAATGAGAGAGATCTCTCGATAGCCAGAGATATCGACTTGTGATGAA 1560
Qy	601 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660		1561 AGGAG 1620
Db	601 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660		1561 AGGAG 1620
Qy	661 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720		1621 GCTAGTGGTATGATGAG 1680
Db	661 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720		1621 GCTAGTGGTATGATGAG 1680
Qy	721 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780		1681 GCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Db	721 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780		1681 GCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Qy	781 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840		1741 TCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db	781 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840		1741 TCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Qy	841 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900		1801 GAGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
Db	841 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900		1801 GAGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
Qy	901 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960		1861 AG 1920
Db	901 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960		1861 AG 1920
Qy	961 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020		1921 ATGATGAG 1980
Db	961 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020		1921 ATGATGAG 1980
Qy	1021 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080		1981 TTGAG 2040
Db	1021 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080		1981 TTGAG 2040
Qy	1081 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140		2041 GAGGAGGCGAGGCTTCCCATAGAGAGCTTGTATCTCGAGAGAGAGAGAGAGAGAGAG 2100
Db	1081 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140		2041 GAGGAGGCGAGGCTTCCCATAGAGAGCTTGTATCTCGAGAGAGAGAGAGAGAGAGAG 2100

[illegible]

1321 TCGATGATCCCAAGCTACATGATGAAGTCAATGTGTGCTCTGATGACGCTT 1380
 QY 1381 GGTAAAGTCTGCGAGTGTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1440
 Db 1381 GGTAAAGTCTGCGAGTGTGCTGCTGCTGCGAGCGCGCGCGCGCGCGCGCG 1440
 QY 1441 AGCTGTCG 1500
 Db 1441 AGCTGTCG 1500
 QY 1501 GTCGTGTCGAAATGAGATGATCTTCGATGACCGCGAAATGACGCTGATGAA 1560
 Db 1501 GTCGTGTCGAAATGAGATGATCTTCGATGACCGCGAAATGACGCTGATGAA 1560
 QY 1561 AGCGAGAGCGTGAAGGTCTTCGAAAGCTGATGATGAGCTGATGAGCTGAGCGGC 1620
 Db 1561 AGCGAGAGCGTGAAGGTCTTCGAAAGCTGATGATGAGCTGATGAGCTGAGCGGC 1620
 QY 1621 GATAGGTGATATTCGAGAGCGTCCGAAAGCGCTCAGCGCTTGGGAGGCACTGATA 1680
 Db 1621 GATAGGTGATATTCGAGAGCGTCCGAAAGCGCTCAGCGCTTGGGAGGCACTGATA 1680
 QY 1681 CGCAGCGCGATGACGCTGCTTAACTAGCGCTCAGCGCTTGGGAGGCACTGATA 1740
 Db 1681 CGCAGCGCGATGACGCTGCTTAACTAGCGCTCAGCGCTTGGGAGGCACTGATA 1740
 QY 1741 TCGCTCTGTCGACCTATGATCGGAGAGGTGGAAGAAATTCATCAAAATATTAAAGAG 1800
 Db 1741 TCGCTCTGTCGACCTATGATCGGAGAGGTGGAAGAAATTCATCAAAATATTAAAGAG 1800
 QY 1801 GAGCTGGGCTTCGAATCAAGCTAGAGAGGTGACAAAGCGCTTATCTTTACAGAGCT 1860
 Db 1801 GAGCTGGGCTTCGAATCAAGCTAGAGAGGTGACAAAGCGCTTATCTTTACAGAGCT 1860
 QY 1861 AAGAAGAGTACGCTGBCCTCTCCGAGAGCGAGGTATATGATGTCGCTTTCAGAGCT 1920
 Db 1861 AAGAAGAGTACGCTGBCCTCTCCGAGAGCGAGGTATATGATGTCGCTTTCAGAGCT 1920
 QY 1921 GTACGTGGCGATGCTGACCTGCGCAGAGCGGTATGATGATGTCGCTTTCAGAGCT 1980
 Db 1921 GTACGTGGCGATGCTGACCTGCGCAGAGCGGTATGATGATGTCGCTTTCAGAGCT 1980
 QY 1981 TTGACACGATGCTGACGAGAGGTGATGATGATGATGATGATGATGATGATGATG 2040
 Db 1981 TTGACACGATGCTGACGAGAGGTGATGATGATGATGATGATGATGATGATGATG 2040
 QY 2041 GAGAGAGCGAGGTGCGATGAGAGGTGATGATGATGATGATGATGATGATGATGATG 2100
 Db 2041 GAGAGAGCGAGGTGCGATGAGAGGTGATGATGATGATGATGATGATGATGATGATG 2100
 QY 2101 GAGAGAGCGAGGTGCGATGAGAGGTGATGATGATGATGATGATGATGATGATGATG 2160
 Db 2101 GAGAGAGCGAGGTGCGATGAGAGGTGATGATGATGATGATGATGATGATGATGATG 2160
 QY 2161 TACCGGTACGCTGAGAGAGGTGATGATGATGATGATGATGATGATGATGATGATG 2220
 Db 2161 TACCGGTACGCTGAGAGAGGTGATGATGATGATGATGATGATGATGATGATGATG 2220
 QY 2221 AGTCAAGAGCGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2280
 Db 2221 AGTCAAGAGCGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2280
 QY 2281 TATGTGACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
 Db 2281 TATGTGACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
 QY 2341 GAGAGAGCGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
 Db 2341 GAGAGAGCGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
 QY 2401 AAGAGAGAGTAA 2412

Db 2401 AAGAGAGAGTAA 2412
 RESULT 3
 DEFINITION
 LOCUS
 AX469431
 Sequence 13 from Patent W00220735.
 ACCESSION
 AX469431
 KEYWORDS
 Pyrobolus fumarii
 Pyrobolus fumarii
 ORGANISM
 Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales; Pyrobolus; Pyrobolus.
 REFERENCE
 Callen, W., Mather, E. J. and Short, J. M.
 Enzymes having high temperature polymerase activity and methods of use thereof
 Pat. No. 0220735-A 13 14-MAR-2002;
 JOURNAL
 DIVERSA CORPORATION (US)
 FEATURES
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SOURCE
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ORGANISM
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 Pyrodicticaceae; Pyrodicticum.
AUTHORS
 Uemori T., Ishino Y., Doi H. and Kato I.
TITLE
 The hyperthermophilic archaeon Pyrodicticum occultum has two
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JOURNAL
 Molecular Microbiology 177 (6), 2164-2177 (1995)
DOI
 10.1046/j.1365-3113.1995.00382.x
PUBLISHED
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FEATURES
 Direct Submission
 Submitted (21-OCT-1994) Yoshizumi Ishino, Takara Shuzo Co., Ltd.,
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gene

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LOCUS

ACCESSION

VERSION

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TITLE

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FEATURES

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ORGANISM Sulfolobus tokodaii; Thermoprotei; Sulfolobales; Sulfolobaceae;
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AUTHORS Kawabayashi, Y., Hino, Y., Horikawa, H., Jin-no, K., Takahashi, M.,
Seah, H., Tanaka, T., Tanaka, K., Okura, K., Nakazawa, H., Takamiya, S.,
Kato, Y., Yoshizawa, T., Tanaka, T., Kudoh, Y., Yamazaki, J.,
Kuehida, N., Oguchi, A., Aoki, K., Maeda, S., Yanagi, M.,
Mishimura, M., Yamagishi, A., Oshima, T., and Kikuchi, H.
Institute of Advanced Industrial Science and Technology, Tsukuba,
Ibaraki 305-0046, Japan
Kawabayashi, Y. and Oshima, T. are at Tokyo University of Pharmacy
and Life Sciences, Hachioji, Tokyo 187-8582, Japan
Evaluation: Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan
Hemology analysis is performed by Smith-Waterman algorithm against
Genbank release 109; EMBL release 56.0; SwissProt release 38.0;
K-mail address for comments and questions: kyuaka@nite.go.jp
ORF organization, sequence alignment and more information are
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303	AGAGATTTTATCTCCACGACCAAGAGTGGTGGTGGAGCTGATCTGGAGTGTATATAC	362
1729	GGTACACAGATCTCGCTCTCTGACCTCTATCCGCGAAGGTGGAGAAATTTCTATCAA	1788
363	GGGACATCTCACTCTCTATCTATCACTCATCAACGACGCGTCTTATGGTCTTATGAA	422
1789	ATTATTAAGAGAGCTGGGTCTTGGATCTCAAGCTAGAGAGGCT	1832
423	CTGGGAAACAAGAGGTCTAAAGGTGGAGGTGATTAATCACTCTATATAGCT	466

RESULT 15
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LOCUS
BF136910 922 bp mRNA linear EST 24-OCT-2000
CGAP L130 Mus musculus cDNA clone IMAGE:4010112 5',
501782103F1 NCI

B136910 GI:1097596
 EST:546910.1
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
 (bases 1 to 922)
 nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgs@leu-nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 Sequencing: Robert Strausberg, Ph.D.
 CNA Library Arrayed by: The I.M.A.G.E. Consortium (ULML)
 DNA Sequencing by: InCyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ULML at:
<http://image.lln.gov>
 f column: 01
 Accession: 580
 High quality sequence from: 580

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Location/Qualifiers	
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Note= "Scanned using Vector NTI Transcriptional Wnt-1 expression driven by Tet-regulated promoter system. Wnt-1 enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.	
Investigator providing samples: Gilbert Smith, NIH	

[illegible]

22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 10:18:29 ; Search time 629 Seconds

10351.122 Million cell updates/sec

Title: US-10-034-849-1

Perfect score: 2412

Sequences: 1 atcgctagagctgtatcc.....tagcagaagaagcagataa 2412

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2412	100.0	2412	26	AA035187
4	2412	100.0	2412	27	AA035187
5	2400.8	99.5	2412	28	AA035187
6	2400.8	99.5	2412	29	AA035187
7	2400.8	99.5	2412	30	AA035187
8	1071.2	41.4	3068	17	AA102574

9 1069.6 44.3 2430 15 AA073844
10 1045.6 43.3 2430 15 AA073843
11 580 24.0 2610 21 AA050678
12 279 11.6 2367 24 AA051883
13 279 11.6 2367 24 AA051887
14 279 11.6 2367 24 AA051887
15 204.2 8.5 2376 18 AA089374
16 200.3 8.3 3321 16 AA089374
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18 191.4 7.9 2325 19 AA054524
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25 167.2 6.9 2411 12 AA05113
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29 161.6 6.7 2325 19 AA056035
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38 123.3 5.1 5255 22 AA050531
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ALIGNMENTS

RESULT 1
AA035187
AA035187 standard; DNA; 2412 BP.
AC AA035187;
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XX 25-JUL-2002 (first entry)
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XX Pyrobolus fumaria DNA polymerase encoding DNA, 1P2.
DE Pyrobolus fumaria DNA polymerase; thermostable; enzyme, gene, ds.
XX
XX DNA polymerase; thermostable; enzyme, gene, ds.
XX
XX Pyrobolus fumaria.
OS
XX
XX Key Location/Qualifiers
XX CDS
XX /tag a
XX /product= "Pyrobolus fumaria DNA polymerase, 1P2"
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XX NC02020735-A2.
XX
XX 14-MAR-2002.
XX
XX 06-SEP-2001; 2001MO-US28007.
XX
XX 06-SEP-2001; 2000US-0655309.
XX
XX (DIVE-) DIVERSA CORP.
XX
XX Callen W, Mathur EJ, Short JM,
XX

P. occultum DNA po
P. abyssal DNA poly
Pyrobolus island
Pyrobolus island
Archaeoglobus lith
DNA encoding Archa
Thermococcus pepco
Thermococcus pepco
Predictum account
Heat-resistant DNA
P. kodakarensis K
DNA for DNA polym
Nucleotide sequenc
T. profundus therm
Pyrococcus abyssi
Pyrococcus abyssi
Thermococcus gorgo
DNA encoding a DNA
Thermococcus gorgo
Pyrococcus gorgo
P. horikoshii DNA e
DNA polymerase gen
KOD1 thermostable
DNA polymerase g
DNA 1P2
Full length heat-r
Pyrococcus kodak
Thermococcus gene
Thermococcus gene
Wild type Pyrococ
Nucleotide sequenc
Pyrococcus furiosu
Pyrococcus furiosu
K110-ococcus furio
P. furiosus (Pfu)
P. furiosus (Pfu)

DR WPI, 2002-362247/39.
XX P-RSDB; AB22118.

New thermostable polymerase useful for sequencing DNA, amplifying
PF nucleotide analog into a DNA molecule, and non-natural nucleotide or a
XX nucleotide analog into a DNA molecule.

Claim 1: Fig 1A-E; 1c1pp; English.

The invention relates to thermostable DNA polymerases having high
temperature polymerase activity, such as those derived from
CC *Pyrobaculum* and nucleic acid molecules encoding such polymerases.
CC Polymerases are useful for catalyzing the formation or repair of a
CC nucleic acid molecule, for example, for sequencing DNA, amplifying
CC nucleotide analog into a DNA molecule, and for incorporating non-
CC amplifying double stranded DNA molecules and for incorporating non-
CC natural nucleotides or nucleotide analogues into a DNA molecule. The
CC present sequence is *Pyrobaculum* fumaric DNA polymerase encoding DNA.

90 Sequence 2412 BP; 631 A; 512 G; 707 C; 562 T; 0 other;

Query Match 100.0%; Score 2412; DB 24; Length 2412;
Best Local Similarity 100.0%; P: No. 0;
Matches 2412; Conservative 0; Mismatches 0; Gaps 0;

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Qy	61	CAAGTATATATATGAGGTTATCTGAGAACGCGAGAGGAGTCTCTATGACAGCT	120
Db	61	CAAGTATATATATGAGGTTATCTGAGAACGCGAGAGGAGTCTCTATGACAGCT	120
Qy	121	TTTGGCCCACTCTCATGCGCTCTTGACCGCGGCGCGATCTTAAAGCAGTAGCA	180
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Db	181	CGTATTGTGTCATTGATGAGGCACAAAGGCCCGATATTAGGTGTAGAGATGCAAGG	240
Qy	241	AAGTACTCTGGAGAGGCTCTGAGGCTCTTACGATTCGACAGCTGCTACCGAGGCTGT	300
Db	241	AAGTACTCTGGAGAGGCTCTGAGGCTCTTACGATTCGACAGCTGCTACCGAGGCTGT	300
Qy	301	AGGGAGTATCGCACTCTGAAGAAGGTTGATGGTGTGAGGATCTTGAAGCGGAT	360
Db	301	AGGGAGTATCGCACTCTGAAGAAGGTTGATGGTGTGAGGATCTTGAAGCGGAT	360
Qy	361	ATAGCTCTATGCTGCTATGCTATGATATGATATATTCCTTACCTGTGATGCT	420
Db	361	ATAGCTCTATGCTGCTATGCTATGATATGATATATTCCTTACCTGTGATGCT	420
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Qy	541	AGGAGAGGCTGAGCCCTCTGAGACAGAGAGGCTCTGCGTGTGAGAGTACTGTT	600
Db	541	AGGAGAGGCTGAGCCCTCTGAGACAGAGAGGCTCTGCGTGTGAGAGTACTGTT	600
Qy	601	GATCTGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	660
Db	601	GATCTGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	660
Qy	661	GAGGCGCAAGAGCGATGAGAAACGATACCGAGCTCTGAGAGTGTGAGAGGATGAC	720
Db	661	GAGGCGCAAGAGCGATGAGAAACGATACCGAGCTCTGAGAGTGTGAGAGGATGAC	720

Qy	721	CCCGCATATATGTCGGTTATACACATCATTTGATTTGGCTTATCTTTTGAAGCGC	780
Db	721	CCCGCATATATGTCGGTTATACACATCATTTGATTTGGCTTATCTTTTGAAGCGC	780
Qy	781	GCGCGCATCTAGGACATTAAGCTGTGATCTAGTAGAGGTGTGGCGGAGCCCACT	840
Db	781	GCGCGCATCTAGGACATTAAGCTGTGATCTAGTAGAGGTGTGGCGGAGCCCACT	840
Qy	841	ATGCTCATGCTGAGGATTAAGCTGTGATCTAGTAGAGGTGTGGCGGAGCCCACT	900
Db	841	ATGCTCATGCTGAGGATTAAGCTGTGATCTAGTAGAGGTGTGGCGGAGCCCACT	900
Qy	901	GAGAGATGCGCGATCTAGGACATTAAGCTGTGATCTAGTAGAGGTGTGGCGGAG	960
Db	901	GAGAGATGCGCGATCTAGGACATTAAGCTGTGATCTAGTAGAGGTGTGGCGGAG	960
Qy	961	ATGAGAGATGCGCGATCTAGGACATTAAGCTGTGATCTAGTAGAGGTGTGGCGGAG	1020
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Db	1021	ATGAGAGATGCGCGATCTAGGACATTAAGCTGTGATCTAGTAGAGGTGTGGCGGAG	1080
Qy	1081	TTAGCCGAGAGATTAAGCTGTGATCTAGTAGAGGTGTGGCGGAGGTCTCCACAT	1140
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Qy	1141	GACGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1200
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Qy	1201	TTTAAAGATGAAGAGCTCTGCGCAGCGGTTTGAGCGCCGAGAGAGACTTACCGTGGC	1260
Db	1201	TTTAAAGATGAAGAGCTCTGCGCAGCGGTTTGAGCGCCGAGAGAGACTTACCGTGGC	1260
Qy	1261	GCTATAGTCTTGAAGCGGTTGAGAGGCTGCGAGATATAGCGTACGCTTACG	1320
Db	1261	GCTATAGTCTTGAAGCGGTTGAGAGGCTGCGAGATATAGCGTACGCTTACG	1320
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Qy	1381	GTTAAAGATGAAGAGCTCTGCGCAGCGGTTTGAGCGCCGAGAGAGACTTACCGTGGC	1440
Db	1381	GTTAAAGATGAAGAGCTCTGCGCAGCGGTTTGAGCGCCGAGAGAGACTTACCGTGGC	1440
Qy	1441	AGGTTGTGCGCGGCTCTTCTCAGACAGCTCTTGAAGAGGCTGTGATGAGCTTGAAGCT	1500
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Qy	1561	AGGTCAGAGAGGCTCTTCTCAGACAGCTCTTGAAGAGGCTGTGATGAGCTTGAAGCT	1620
Db	1561	AGGTCAGAGAGGCTCTTCTCAGACAGCTCTTGAAGAGGCTGTGATGAGCTTGAAGCT	1620
Qy	1621	GTCGTCGTGAGAGAGGCTCTTCTCAGACAGCTCTTGAAGAGGCTGTGATGAGCTTGAAGCT	1680
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Db	1681	CCACAGCGCTCAAGATGATCTTGAAGAGGCTCTTGAAGAGGCTGTGATGAGCTTGAAGCT	1740
Qy	1741	TGCTCTCTGTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1800
Db	1741	TGCTCTCTGTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1800
Qy	1801	GAGCTGCGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCT	1860

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 Db 1321 TCGATGTACCAAAACATCATGAATAAGTACAATGTGCTCTGACACGCTGTGAGCGCT 1380
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 AC ASK14892;
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 DT DNA encoding Pyrobolus thermostable DNA polymerase protein #3.
 XX Gene; da; thermostable; DNA polymerase; DNA repair;
 XX polymorphism identification.
 XX Pyrobolus fumarius.
 XX Key
 XX Location/Qualifiers
 XX CDS
 XX /tag a
 XX /product="Pyrobolus DNA polymerase"
 FT US2002132243-A1.
 XX
 XX 19-SEP-2002.
 PD 06-SEP-2001; 2001US-0948359.
 XX
 XX 06-AUG-1997; 97US-0907166.
 PR 07-SEP-1999; 99US-0391340.
 PR 06-SEP-2000; 2000US-0656209.
 PA (CALL// CALLEN W.
 PA (MATH// MATHUR E J.
 PI (SHORT// SHORT J.
 PI Callen W, Mathur EJ, Short J;
 WP1: 2003-182285/18.
 PR P-FSDB; AB876153.
 DR
 DR Novel DNA polymerases having increased activity and stability at
 PT increased pH and temperature, useful for DNA sequencing, amplification
 PR and incorporating non-natural nucleotides or nucleotide analogs -
 XX Claim 42; Page 52-54; 81pp; English.
 CC This invention relates to a novel purified polypeptide derived from
 CC Pyrobolus fumari which has thermostable DNA polymerase activity. The
 CC polypeptide is useful for catalyzing the formation of
 CC repair of a nucleic acid sequence and for identifying polymorphisms. The nucleic
 CC reference sequence and for identifying polymorphisms. The nucleic
 CC acid sequence of the invention is useful for preparing cDNA from mRNA,
 CC the amplification process of double-stranded DNA molecule.
 CC The nucleic acid sequence of the invention is useful for preparing a
 CC nucleotide or its analogues into a DNA molecule, by contacting a
 CC polypeptide encoded by the nucleic acid with a DNA template in a PCR
 CC amplification reaction. The nucleotides which may be used for this are
 CC dNTPs, dNTPs, or nucleotides. The nucleic acid probe
 CC derived from the nucleic acid sequence of the invention is useful in
 CC chromosome walking procedures to identify clones containing genomic
 CC sequences located adjacent to a sequence of the gene encoding the DNA
 CC polymerases of the invention. Such methods allow the isolation of the
 CC genes which encode additional proteins from the host organisms. The

CC Polymerase of the invention have increased activity and stability at
 CC increased pH and temperature, and high processivity. The present
 CC sequence represents a DNA sequence encoding a Pyrobute kumaris
 CC thermostable DNA polymerase protein of the invention.

SC Sequence 2412 BP; 627 A; 513 C; 712 G; 560 T; 0 other;

Query Match 99.5%; Score 2400.8; DB 25; Length 2412;
 E-Value 0.0; Percent Identity 99.5%;
 Match 2405; Conservative 7; Indels 0; Gaps 0;

1 ATGACGAGGATGATTCAGCGGTTTGAAGCTTTCAGCTTACGAGGATGCTGTTGAAGAGCT 60
 Db 1 AAGACGAGGATGATTCAGCGGTTTGAAGCTTTCAGCTTACGAGGATGCTGTTGAAGAGCT 60
 Qy 61 CAGGATCATATCGGATATCTCGAGAGCGCGAGGAGGATGCTTCAATGAGAGCT 120
 Db 61 CAGGATCATATCGGATATCTCGAGAGCGCGAGGAGGATGCTTCAATGAGAGCT 120
 Qy 121 TTTCGCGCATCTTATAGGCTGCTTTCACCGGCGCGATCTTAACCGGTAGACAA 180
 Db 121 TTTCGCGCATCTTATAGGCTGCTTTCACCGGCGCGATCTTAACCGGTAGACAA 180
 Qy 181 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 181 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Qy 241 AAGTACTTTCGAGAGCGCTGAGGCTTACGATGATGATGATGATGATGATGATGATGAT 300
 Db 241 AAGTACTTTCGAGAGCGCTGAGGCTTACGATGATGATGATGATGATGATGATGATGAT 300
 Qy 301 AGGAGATATCGCAACTGTAAGAGACTGTGATGATGATGATGATGATGATGATGATGAT 360
 Db 301 AGGAGATATCGCAACTGTAAGAGACTGTGATGATGATGATGATGATGATGATGATGAT 360
 Qy 361 ATACGCTTCGCTATCGCTATCTCATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 ATACGCTTCGCTATCGCTATCTCATGATGATGATGATGATGATGATGATGATGATGAT 420
 Qy 421 GTAGAGCGTACGCGCTTCGAGAACGAGTGGCTTCGCTGATGATGATGATGATGATGAT 480
 Db 421 GTAGAGCGTACGCGCTTCGAGAACGAGTGGCTTCGCTGATGATGATGATGATGATGAT 480
 Qy 481 AAGAGCGCGCGAGCGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 481 AAGAGCGCGCGAGCGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Qy 541 AGGATATCGGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 541 AGGATATCGGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Qy 601 GATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 Db 601 GATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 Qy 661 GAGCGCGAGCGCTACAAAACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 Db 661 GAGCGCGAGCGCTACAAAACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 Qy 721 CCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 Db 721 CCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 Qy 781 CCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 Db 781 CCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 Qy 841 AGGATATCGGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Db 841 AGGATATCGGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Qy 901 GAGAGATTCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 Db 901 GAGAGATTCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960

901 GAGAGATTCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 Qy 961 ATGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Db 961 ATGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Qy 1021 CCGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 Db 1021 CCGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 Qy 1081 TCCAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 Db 1081 TCCAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 Qy 1141 GACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 Db 1141 GACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 Qy 1201 TTGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 Db 1201 TTGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 Qy 1261 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 Db 1261 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 Qy 1321 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 Db 1321 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 Qy 1381 GTGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 Db 1381 GTGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 Qy 1441 GGTAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Db 1441 GGTAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Qy 1501 GTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 Db 1501 GTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 Qy 1561 AGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 Db 1561 AGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 Qy 1621 GGTAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 Db 1621 GGTAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 Qy 1681 CCGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 Db 1681 CCGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 Qy 1741 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
 Db 1741 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
 Qy 1801 GAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 Db 1801 GAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 Qy 1861 AAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 Db 1861 AAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 Qy 1921 GTAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 Db 1921 GTAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 Qy 1981 TTGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 Db 1981 TTGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040

XX (DIVE)- DIVERSA INC.
 PA Callen W, March 82;
 XX P-F8DB; AAT00937.

DR WPI: 1999-180490/15.
 XX P-F8DB; AAT00937.

XX DNA polymerases from extremely thermophilic bacteria - useful for
 XX DNA synthesis

XX Claim 3: Fig 3; 72pp; English.

XX This sequence encodes a DNA polymerase of the invention, that was
 CC isolated from thermophilic bacteria. The polymerase is a DNA
 CC enzyme and as such is useful for DNA synthesis. The polymerase
 CC purification and to screen for related enzymes). Fragments of the DNA
 CC encoding the polymerases are used as probes to isolate related or
 CC homologous polymerases. The polymerase is a DNA polymerase that
 CC the 3' end of a polynucleotide chain, using a complementary
 CC polynucleotide strand as a template. The polymerases have optimum
 CC activity at over 80 deg. and can maintain and regain activity after
 CC exposure to temperatures above 70 deg. C.

XX Sequence 2367 BP; 799 A; 417 C; 612 G; 539 T; 0 other;

XX Query Watch 11.4%; Score 279; DB 20; Length 2367;
 XX Best Local Similarity 50.9%; Pred. No. 1.9e-75; Indels 63; Gaps 7;
 XX Matches 889; Conservative 0; Mismatches 795;

XX 530 TTCCCGACCTGACGACCTGCGCTTCATATGAGGTTTATAGCAGCAGGCTGCGCC 589

XX 488 TTCCCGACCTGACGACCTGCGCTTCATATGAGGTTTATAGCAGCAGGCTGCGCC 547

XX 590 GTCCGACGCGGCTCTGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643

XX 548 ATCCGACGCGGCTCTGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607

XX 650 TATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709

XX 608 TCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 658

XX 710 AAGGATGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769

XX 659 GCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718

XX 770 TTTCGACGCGGCTCTGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 829

XX 719 TCAAGGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 778

XX 830 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 889

XX 779 TGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 832

XX 890 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 949

XX 833 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892

XX 950 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009

XX 893 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 952

XX 1010 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069

XX 953 CATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1013

XX 1070 CTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1129

XX 1004 ACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063

XX 1130 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189

DB 1064 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123

QY 1190 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1249

DB 1124 TAAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1180

QY 1250 CTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1309

DB 1181 GTATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1240

DB 1210 TCAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1369

DB 1241 TCAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1300

QY 1370 TTTCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1429

DB 1301 TTTCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1348

QY 1430 TCAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1489

DB 1349 ACAAATTCAGAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1408

QY 1490 TTTCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1549

DB 1409 TCAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1468

QY 1550 TTTCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1609

DB 1469 TCAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1528

QY 1610 TTTCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1669

DB 1529 GGTGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1588

QY 1670 GGTGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1729

DB 1589 GGTGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1648

QY 1730 GTGACGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1789

DB 1649 GGTGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1708

QY 1790 TATGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1828

DB 1769 TATGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1728

QY 1829 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1888

DB 1769 TATGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1825

QY 1889 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1948

DB 1826 TATGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1885

QY 1949 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2008

DB 1886 TATGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1945

QY 2009 TATGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2068

DB 1946 TCAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2005

QY 2069 TTTCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2128

DB 2006 TATGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2065

QY 2129 TTTCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2188

DB 2066 TATGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2125

QY 2189 GTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2248

DB 2126 GTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2185

QY 1790 TTATTAAT...GGAGGAGCTGGGTTTCAAAATCAGTACGAGA 1828
 DB 1709 AAGTTTAAAGCTCATAGTAACTTTCGAGAGGATTCGCAATACAGAGATAGTGT 1768
 QY 1829 AGGTGTCAAAAGCTTATTTTACAGAGGCTTAAGAGAGATAGTGTGGCTTCTGAGG 1888
 DB 1769 AATCTCAAGAGCAATTTCTTCCTGGA...AGGAAAGATATGCTGGATATGACACAG 1825
 QY 1889 ACGGAGCTATATAGTATTTGCGTTTCGAGAGTCTAGTGGCATGTGTGAACTGCCA 1948
 DB 1826 ATGAGAGATATGTTAAAGGCTTCTTAAGTCTGAGAGAGGAGCTGTGCGAGCTGCA 1885
 QY 1949 ACGAGGTTCAAGCTTAGGTTGTGAAATGATATGAGAGAGTGTGAGTCAACAGCTG 2008
 DB 1886 AGAGATATGAGAGGCTGTATTAATATCTTGAAGAGAGAGATCTCGTAAAGAGCTG 1945
 QY 2009 TAGAGTATCTAGAGAGATTTGAAAGAGGTTGAGAGAGGCTGAGGTTTCCATATGAGAGC 2068
 DB 1946 TTGATATTTTGAAAGGATCATAGAGAGAGTAAAGAGGAGCAAAATTCGCTTGAAGATT 2005
 QY 2069 TGTATATCTGGAAGGCTTATAGAGGCTTCTGAGATGATACAGAGGAGAGCTGACAG 2128
 DB 2006 ATATCATCTACAGAGGATTTAGAGAAACATCAAGATGACAGATGTACAGCTCATG 2065
 QY 2129 TCGTTCGAGAGAGAGAGGCTCTGTTCAGAGCTACCGGTATACGCCAGAGCAAGATG 2188
 DB 2066 TAAAGGCTGCTAGAGAGGCGGCAAGAGAGATATGATACAAATCGCTCAAGAGCTG 2125
 QY 2189 GGTATATGATATGAGAGGCTGTCGCTATCTAGTCAAGAGAGATGATGATCTATGAG 2248
 DB 2126 GTTTTGTGTACAAAGGTTGTGGAGAGTATAGTATAGGCTTTTCTCTCTGATCTCA 2185
 QY 2249 TCAAGCA 2255
 DB 2186 TACAGCA 2192

RESULT 14

ID ABX14887 standard; DNA; 2367 BP.
 XX ABX14887

XX ABX14887;
 DT 08-APR-2003 (first entry)

XX DNA encoding Archaeoglobus thermostable DNA polymerase protein.
 XX Gene; ds; thermostable; DNA polymerase; DNA repair;
 KW polymorphism identification.

XX Archaeoglobus lithorhophilus.
 PH Key Location/Qualifiers
 FT COS 1..2367
 FT /*csg-
 FT /*product= "A. lithorhophilus DNA polymerase"

US200112243-A1.

XX 19-SEP-2002.

PF 06-SEP-2001; 2001US-0948369.

XX 06-AUG-1997; 97US-0907166.

PR 07-SEP-2000; 2000US-0655109.

XX 06-SEP-2000; 2000US-0655109.

XX (CALL) CALLEN W.

PA (SHORT) MATHUR E J.

XX (SHORT) SHORT U.

XX Callen W, Mathur EJ, Short U;

XX

DR WP1; 2003-182285/18.

DR P-PSDB; AB073156.

XX Novel DNA polymerases having increased activity and stability at
 XX increased pH and temperature useful for DNA sequencing
 XX and incorporating non-natural nucleotides or nucleotide analogs.
 XX Claim 1, Page 38-39; 81pp; English.

XX This invention relates to a novel purified polypeptide derived from
 XX Pyrobolus fumari which has thermostable DNA polymerase activity. The
 XX protein of the invention is useful for catalyzing the formation of
 XX a double-stranded DNA molecule. The polypeptide of the invention is
 XX a reference sequence and for identifying polypeptides having a
 XX acid sequence of the invention is useful for preparing cDNA from mRNA,
 XX and in an amplification process of a double-stranded DNA molecule.
 XX The sequence is also useful for incorporating non-natural
 XX nucleotides or analogs into a DNA template using PCR
 XX amplification reaction. The nucleotides which may be used for this are
 XX inosine, 2-aminopurine or 5-methylcytosine. A nucleic acid probe
 XX complementary to the sequence of the invention is useful in
 XX chromosome walking procedure to identify chromosomal
 XX sequences located adjacent to a sequence of the gene encoding the DNA
 XX polymerases of the invention. Such methods allow the isolation of
 XX polymerases of the invention having the same or the most organismal
 XX increased pH and temperature, and high processivity. The present
 XX invention represents a DNA sequence encoding an Archaeoglobus
 XX lithorhophilus thermostable DNA polymerase protein of the invention.

XX Sequence 2367 BP; 799 A; 417 C; 612 G; 539 T; 0 other;

Query Match 11.6%; Score 279; DB 25; Length 2367;
 Percent similarity 50.9%; Pred. No. 1.9e-75;
 Matches 889; Conservative 0; Mismatches 755; Indels 63; Gaps 7;

QY

DB

QY

DB

QY

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QY

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QY

DB

QY

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QY

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QY

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DB

QY 1070 CTACTTACGGCTTACGCGAGAGATATTCGGTTCGATCATCGTTCGCGATACAG 1129
 DB 1040 ACGCTGACTTACCTAGCTAGAGATTCGCTCCCATCATGATTAAGAGCTTCCAGATACG 1063
 QY 1130 GTCTCTCCATCTACGCTAGAGATTCGCTCCCATCATGATTAAGAGCTTCCAGATACG 1189
 DB 1104 GATATCTCTCGATATGATGTCAGAGAGCGGAGAGTAACTGATGATGCTGCTGT 1123
 QY 1190 TACCGCGCGGCTTAAATTAAGAGCTTCGCGACACCGCTGAGCGCGCCAGAGAGA 1249
 DB 1124 TAACTGCAAGCGACAAATCTGCGCACTTCGACCCACCCCGAGAG...ATGCGCGACA 1180
 QY 1250 CTATCGCTGCGCTGATGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 1309
 DB 1181 GCTATGAGAGAGCATTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 1240
 QY 1310 TCGATCTGAGCTGCTGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1369
 DB 1241 TGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1300
 QY 1370 TCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1429
 DB 1301 TCTG...-----AAATGAGCAATGCGCAATTCATGATGCTGCGCTGCGCTG 1348
 QY 1430 ACGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1489
 DB 1349 ACGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1408
 QY 1490 TCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
 DB 1409 AAGAGAGAGAGAAATAGAGAGCTTATGAAACACTTGACTCAATCGCGAGATTAAG 1468
 QY 1550 TCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1609
 DB 1469 TCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1528
 QY 1610 GTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1669
 DB 1529 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1588
 QY 1670 GCGCTCTATACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1729
 DB 1589 GAGCTCTTATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1648
 QY 1740 GCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1789
 DB 1639 GCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1708
 QY 1790 TTTTAA...-----GGAGAGCTGGGCTGCAATCAAGCTGAGGA 1828
 DB 1709 AAGTAAAGCTCTAGTAAATCTTCGAGAGAGATTCGCAATCAAGCTGAGGA 1768
 QY 1829 AGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1888
 DB 1769 AAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1825
 QY 1889 ACGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1948
 DB 1826 ATGAGAGATCTTAAAGGCTCTTAAAGGCTCTTAAAGGCTCTTAAAGGCTCTTAA 1885
 QY 1949 AGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2008
 DB 1886 AAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1945
 QY 2009 TAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2068
 DB 1946 CTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2005
 QY 2069 TTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2128
 DB 2006 KATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2065

QY 2129 TCGTTCGCGAGAGAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2188
 DB 2066 TAAAGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2125
 QY 2189 GGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2248
 DB 2126 GTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2185
 QY 2249 TCAAGCA 2255
 DB 2186 TAGAGCA 2192
 RESULT 15
 AAT88374 standard; cDNA; 2376 BP.
 ID AAT88374
 XX AAT88374;
 XX AAT88374;
 DT 28-JUN-1998 (first entry)
 XX Thermococcus peptonophilus SM-2 thermostable DNA polymerase cDNA.
 XX JCM 9654; thermostable; DNA polymerase;
 KW nucleic acid sequence amplification; PCR; ds.
 KW Thermococcus peptonophilus.
 OS Thermococcus peptonophilus.
 XX Key Location/Qualifiers
 FH COS 2...2325 a
 FT /product= DNA_polymerase
 XX JP09252776-A.
 PD 30-SEP-1997.
 XX 19-MAR-1996; 963P-0063112.
 PR 19-MAR-1996; 963P-0063112.
 XX (TOYO) TOYOBO KK.
 PA NPI, 1997-530149/49.
 DR P-P5DB; 1997-530149/49.
 XX Thermococcus peptonophilus thermostable DNA polymerase - useful for
 XX nucleic acid sequence amplification, e.g. PCR.
 XX Claim 13; Pages 19-22; 27pp; Japanese.
 PS The present sequence encodes a Thermococcus peptonophilus SM-2
 CC (JCM 9654) derived thermostable DNA polymerase, which can be used
 CC for nucleic acid sequence amplification, e.g. PCR.
 SQ Sequence 2376 BP; 679 A; 546 C; 693 G; 458 T; 0 other;
 Query Match 8.5%; Score 204.2; DB 18; Length 2376;
 Best Local Similarity 48.5%; Pred. No. 3.5e-52;
 Matches 892; Conservative 0; Mismatches 849; Indels 69; Gaps 8;
 QY 622 GTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 567
 DB 608 GTATACCGGATTTGTAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561
 QY 692 GTATACCGGATTTGTAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
 DB 569 ATGTATAGAGGCTTCTCGAGTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 627
 QY 742 AACAAACATTCATTCGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 801
 DB 628 ACGGTGATCATCTTGCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTC 687

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Oy 802 CTGAGTGTACAGAGGTGCGCGGACCCACACCTAGCTGATCATGCGCAGCTCT 861
Db 688 TTTCCTCTCGAAGGACGAGAGGAGCCCTAAAGTTCAGAGAGGTGGCGATGTTGCT 747
Oy 862 GTCCCTCGCGGCTTAAGCTAGATCTGTACACTATGCCGAGAGGTGCGAGAGTCAG 921
Db 748 GTGAGGTGTAGGCGAGAGTACACTTGTATCTACCCCTGTGTAAAGCGAGGTAAAC 807
Oy 922 ATAAAGGTCGTGCGAGAGGTGCGAGAGTCTGAGAGTCTGAGAGCGAGGTGAAGCG 861
Db 808 CTCCCAACATATACGCTTGAGGCTGTCTGTAAAGCATCTTGGAGAG--CMAAGG 864
Oy 962 ATCTCTCATGTGTGAGATATCCAGCATATTCGAGTCCGACCGGAGAGAGACACATTA 1041
Db 865 AAGGTCTACCGCGAGAGATACACACCGCTCTGAGAGCGAGGAGGCTTGAGAGGTA 924
Oy 1042 CTCTGAGCGCGCGCGCGAGGTGCGCGCTCTCTATAGGCTTACCGGAGAGATATTCG 1101
Db 925 CTCTAAATATCTATGAGAGAGCCCAAGGTATCTTAAGAGCTGGAAGAGATGTTCCG 984
Oy 1102 TTGTCTATCTGTTGTGTAATACAGATCTCCATAGACCTGTAGTGTGAGTGTAGT 1161
Db 985 ATGAGGCGCAGCTTTCGCGCTGTATCGCGCTGCTCTGAGAGTCTTCGCGCTACG 1044
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Oy 1222 CGAAGCCGCTGTAGCGCCGCAAG--NAGCTACGTGCGCTATA 1266
Db 1105 CTGACAGCCCTGAAGAGGCTGTGCGAGAGCGCAGCTGTGAGAGGGGCTAC 1164
Oy 1267 GTTCTGTAGCCGCTGTAGAGGCGGTGACAGAGATATAGCCGTACTCGACTTAGCTGATG 1326
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Oy 1387 AAGTGTGCGAGTGTGTGCTGGAGCGCCCGAGGCTGACGACGATGTTCTGTAGTGT 1446
Db 1285 AAGAGTATGACACT--CCGCCCATGTTGGCCAGCGCTTCTGCAAGAC 1332
Oy 1447 CGCGCGGCTCTTGAGAGCTGTGAGAGCTGTGAGATCTGTAAAGCTGTGCTGT 1506
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Oy 1507 GCTGAATGAGAGATATCCCGGATGAGCCAGATATCGATGTGTGAGTAAAGGAG 1566
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Db 1590 ATCAATTACATATCAACAGCTTCCTGAGTGGCTGTGTGAGCTGTGATGAGAGGTTTAC 1749
Oy 1837 AAGCGCTTATCTTACAGAGGCTAAGAGAGTATGCTGCGCTTCTCGAGAGAGAGCT 1896

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Search completed: November 26, 2003, 12:25:11

Job time : 635 secs

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RESULT 3

/ US-09-948-369-13
 / Sequence: US0900013224311
 / GENERAL INFORMATION:
 / APPLICANT: DIVERSA CORPORATION
 / APPLICANT: CALLER, Naiter
 / TITLE OF INVENTION: ENZYMS HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY AND METHODS
 / TITLE OF INVENTION: THEREOF
 / FILE REFERENCE: DIV1150-3
 / CURRENT PILING DATE: 2001-09-06
 / PRIOR APPLICATION NUMBER: US 09/456,309
 / PRIOR PILING DATE: 2000-09-06

/ PRIOR APPLICATION NUMBER: US 09/391,340
 / PRIOR PILING DATE: 1997-08-06
 / NUMBER OF SEQ ID NOS: 16
 / SEQ ID NO 1: Patent version 3.0
 / SEQ ID NO 13
 / LENGTH: 2412
 / TYPE: DNA
 / ORGANISM: Pyrobolus fumarius
 / US-09-948-369-13
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 Best Local Similarity 100.0%; Freq. No. 0;
 Matches 2412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 481 FAGAGGCTTCGCTATTCATTCAGATTCAGAGCTTCAGAGCTTCAGAGCTTCAGAGCT 540
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9. DISCUSSION

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US-10-029-382-1
; Sequence 1, Application US/10029382
; Publication NO. US20020164619A1
; INVENTOR: MATHUR, ERIC
; APPLICANT: CALLEEN, Walter
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: CALLEEN, Walter
; APPLICANT: MATHUR, ERIC
; TITLE OF INVENTION: ENHANCED
; FILE REFERENCE: DIVER1350-2

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RESULT 7

US-09-948-369-15
 / Patent No. US200323243A1
 / GENERAL INFORMATION:
 / APPLICANT: DIVERSA CORPORATION
 / INVENTOR: KATZ, Walter
 / APPLICANT: KATZ, Walter
 / TITLE OF INVENTION: ENZYMES HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY AND METHODS
 / FILE REFERENCE: DIVER1350-3 US/09/948,369
 / CURRENT FILING DATE: 2001-09-06
 / PRIOR FILING DATE: 2000-09-06
 / PRIOR FILING DATE: 1999-09-07
 / PRIOR APPLICATION NUMBER: US 09/656,309
 / PRIOR APPLICATION NUMBER: US 08/907,166
 / PRIOR APPLICATION NUMBER: 1997-08-06
 / SEQ ID NO: 16
 / SOFTWARE: PyroClobus version 3.0
 / SEQ ID NO 15
 / LENGTH: 2412
 / TYPE: DNA
 / ORGANISM: Pyrococcus furiosus
 US-09-948-369-15

Query Match 99.5%; Score 2400.8; DB 10; Length 2412;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2409; Conservative 0; Mismatch 7; Indels 0; Gaps 0;

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Qy 2401 AAGACAGATGA 2412
Db 2401 AAGACAGATGA 2412

RESULT 8
US-09-391-340-5
; Sequence 5, Application US/09391340A
; Patent No. US20020013455A1
; GENERAL INFORMATION: Walther
; APPLICANT: Walther, Eric
; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF NOVEL POLYMERASES
; FILE REFERENCE: 09010/027001
; CURRENT PILLING DATE: 08/09/99/391.340A
; EARLIER APPLICATION NUMBER: US 08/907,166
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5: seq5sq for Windows Version 3.0
; LENGTH: 2367
; TYPE: DNA
; ORGANISM: Archaeoglobus lithotrophicus
; NAME/KEY: QDS
; LOCATION: (1)...(2364)
US-09-391-340-5

Query Wasch 11.6%; Score 279; DB 9; Length 2367;
Best Local Similarity 50.3%; Pred. No. 4.1e-80;
Matches 889; Conservative 0; Mismatches 795; Indels 63; Gaps 7;

Qy 530 TTCGGGATCTGGATGACTGCGCTTCCGATTCGATGATGATGATGATGATGATGATGATG 589
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Qy 590 GTCCGACCGCGATCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 649
Db 548 ATCCGACGAGATCTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 607
Qy 650 TATTCATCTCGAGGCGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 709
Db 608 TCACGGTG-----ATACGAGAGAGATGCTTACGATGATGATGATGATGATGATGATTC 658
Qy 710 AGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 769
Db 659 GCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 718
Qy 770 TTTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 829
Db 715 TCAGAGAGAGATGCGAGAGATGCGAGAGATGCGAGAGATGCGAGAGATGCGAGAGATGCG 778
Qy 830 ACCGACCACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 889
Db 775 TGGCTATCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 832
Qy 890 ACGATATCTCGGAGAGAGATGCGAGATGCGAGATGCGAGATGCGAGATGCGAGATGCGAG 942
Db 831 ATGATATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 892
Qy 950 ATCTAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1009

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QY 1837 AAAGCTATTTCTTACAGAGCTTAAGAGAGTACCTGGCTCTCTGAGAGAGAGCT 1896
 DB 1750 AAAGCGGCTCTCTC---GTCAGAGAGAGAGATATCGTGTATAGAGAGAGAGAGAG 1806
 QY 1897 ATGATATATGCGTGTCTGAGAGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAG 1956
 DB 1807 ATAAACACCGCCGAGCTATAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1866
 QY 1957 CAGACTATAGCTTCTGAAATATATATATATATATATATATATATATATATATAT 2016
 DB 1867 CAG 2016
 QY 2017 GTACAG 2076
 DB 1927 GTACAG 2136
 QY 2077 TCGAG 2186
 DB 1987 CAG 2046
 QY 2137 CAG 2196
 DB 2047 CCGAG 2206
 QY 2197 ATAGTATAG 2256
 DB 2107 GTGCTTACAG 2166
 QY 2257 CAG 2313
 DB 2167 ACAG 2226
 QY 2314 AAG 2352
 DB 2227 AGATATCTGAG 2265

RESULT 13

US-10-227-110-97

Sequence 97, Application US/10227110

Publication No. US2003013577A1

GenBank Accession No. AF000001

APPLICANT: Statagene

TITLE OF INVENTOR: HIGH FIDELITY DNA POLYMERASE COMPOSITIONS AND USES THEREFOR

FILE REFERENCE: 25436/2155C US/10/227,110

CURRENT FILING DATE: 2002-08-23

PRIOR APPLICATION NUMBER: 10/079,241

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: 10/080,508

PRIOR FILING DATE: 2002-07-30

PRIOR APPLICATION NUMBER: 10/035,091

PRIOR FILING DATE: 2001-12-21

INVENTOR: Statagene, Inc. d/b/a: 128

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 97

LENGTH: 2325

ORGANISM: Pyrococcus sp.

US-10-227-110-97

Query Match 7.9%; Score 189.8; DB 12; Length 2325;

Similarity 41.9%; Gaps 85; Mismatches 857; Indels 69; Gaps 8;

Matches 853; Conservative

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DB 508 GTGAG 567

QY 682 CCGATACCGAG 741

DB 568 ATGATATAG 627

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 DB 628 AACGCGGAGCACTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 697
 QY 802 CTTCATTTGATCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 861
 DB 688 TTTCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 747
 QY 862 GTTCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 921
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 QY 982 ATGAG 1041
 DB 865 ATGAG 924
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 DB 1105 CCGAG 1164
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 DB 1165 GTTAAAG 1224
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 QY 1387 ATGAG 1446
 DB 1285 ATGAG 1332
 QY 1447 CCGCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1506
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 QY 1507 GTTCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1566
 DB 1390 ATGAG 1449
 QY 1567 ATGAG 1626
 DB 1450 ATGAG 1509
 QY 1627 GTTCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1686
 DB 1510 GTTCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1569
 QY 1687 CCGATCA---ACTTATGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1743
 DB 1570 ACTTATGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1629
 QY 1744 CTTCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1803
 DB 1630 TTTTTCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1689
 QY 1804 CTGCGCTT-----TCGAAATCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1836


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1804 CTGGGGT-----TGGAAATGAGCTAGAGAGGTATC 1836
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Db 1750 AAAGCTTTCTTTC-----GTCCAGAGAGAGTATCGGTGTAGAGAGAGAGCG 1806
Qy 1897 ATAGATATATGTCGTATCGAGGCTATCGTGGCAATATCGGTGTAGAGAGAGCT 1956
Db 1807 ATACAGCCCGGAGCTTGAGATATGAGGTGTGAGCTGAGAGAGAGTACGAGAGAG 1866
Qy 1957 CAGCTAAGTGTGTGAAATATGATTAAGACGAGTGAAGTGAACAGAGCTGTAGATAC 2016
Db 1867 CAGCGAGGGTGTGTGAGGCTTGTCTAAAGAGCGAGCTGTGAGAGGCGCTGAGATA 1926
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Qy 2077 TGGAGAGCCCTTAGTAGGCTCTGAGAGTGAACAGAGCGACACAGCTGTGTCCA 2136
Db 1987 CAGAGCAGATATGTCGAGAGCTGTGAGGCTTAAAGAGCTTCCCAAGCTGTCCCTT 2046
Qy 2137 CAGAGAGATCTGTGAGAGCTGTGAGGCTTAAAGAGCTTCCCAAGCTGTCCCTT 2136
Db 2047 GCGAAGAGTGTGCGCGAGAGAGTCAAAATATGCGCTGAGAGCTGAATCAATC 2106
Qy 2197 ATAGTGAAGTGTGGCGGTGTGCTGTGAGAGAGAGAGAGAGAGAGTGTCTATGAT 2256
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Qy 2257 GTACAGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2313
Db 2167 ACGAGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2226
Qy 2314 AGATATGAGTACTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2352
Db 2227 AGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2245

RESULT 15
; US-10-227-110-98
; Sequence 98, Application US10227110
; Publication No. US2003014357A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: HIGH FIDELITY DNA POLYMERASE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 25436/2155C
; CURRENT APPLICATION NUMBER: US/10/227,110
; PRIORITY NUMBER: 10/075,241
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 2002-02-20
; PRIOR FILING DATE: 2002-07-30
; PRIOR FILING DATE: 2002-07-30
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2325
; LENGTH: 2325
; TYPE: DNA
; ORGANISM: Pyrococcus sp.
; REMARK:
; FEATURE: misc feature
; LOCATION: (1150)..(1152)
; OTHER INFORMATION: As at positions 1150-1152 may be any nucleotides so that the code
; OTHER INFORMATION: n at 1150-1152 encodes for Asn, Leu, His, Gln, or Ser.
us-10-227-110-98

Query Match 7.8t; Score 188.4; Db 12; Length 2325;
Best Local Similarity 47.8t; Pval: 2.5e-50;
Matches 81; Conservative 0; Mismatches 859; Indels 69; Gaps 8;

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622 GTGAACTACGACGTCGATATGAGTGTCTATTCATTCGAGAGGCGAAGACATCGAAA 681
Db 508 GTGTACTTGGAGAGATGTGATCTCCCTAACTTGAATCTCTCGACGGAGAGAG 567
Qy 682 CGGATACGCGAGTTGTAGATATCGTGAAGAGGTATGACCCCGACATATAGTCGGTAT 741
Db 568 ATGAAAGGCGCTCTCCGTTGTGTGGAGAGAGAGCGAGGTCTCTATACCTAC 627
Qy 742 AACACATCATTTGGATTGGCTTATCTTTTGAAGGCGCGCGCATCTTAGGACATAAG 801
Db 628 ACGCGACGACCTCTCCGTTGTGTGGAGAGAGAGCGAGGTCTCTATACCTAC 687
Qy 802 CTGTGATGATCAGAGAGTGTGTGTGCGGACCGACCATAGCTGACATAGCGCATCT 861
Db 688 TTCCCTCTCGAAGGAGATGAGAGCGAGCCCGAGATCTAGAGAGATGGCGACAGT 747
Qy 862 GTCTCTGCGAGGCTTAAGCTAGATCTGTAGCATCTATCCGAGAGATGCGAGATCAG 921
Db 748 GTGAGATGTAGGAGGCGAGATACACTTGCATCTCTATCTGTGTATAGACGACAT 807
Qy 922 ATTAAGATGTCTGAGAGAGTGTGCGAGATATCTAGCGGTGTGAGAGAGATGTAG 981
Db 808 CTGCGCCATACACCTCTGAGCGCTGTTTATGAGAGCTCTCTCGCTACCGAA...GAG 864
Qy 982 ATCTCAATTTGTGAGATCTGAGCTATCTGAGAGAGATGCGAGAGAGACGCTATTA 1041
Db 865 AAGGTTTATGCTGTGAGAGATTAACACGCTCTGAGAGAGAGAGAGAGAGAGAGAG 924
Qy 1042 GTTCATTCGAGTGTGAGAGAGTGTGCGGCTGTGAGAGAGAGAGAGAGAGATTTGG 1101
Db 925 GCGCGCTACTGATGAGAGATGAGAGGTCAATACGAGCTGTGAGAGAGAGTCTCTCG 984
Qy 1102 TTCTCTATTCGATGTGTGATACAGTCTATCTCCACTACAGAGTGTAGTGGATGT 1161
Db 985 ATGAGAGCGCTGAGCTTCTCGCTTATCGGCGAGTCTCTGTGAGAGCTCTCGG 1044
Qy 1162 GTTGGTTTGTGACTGTGATGTACTATACGCGCGGCTTAAAGATGAAAGAGCTTGG 1221
Db 1045 ACTGCAACTCGCTTGTGTGTTTCTCTCGAAGAGCTTATGAGAGATGGAGTGGC 1104
Qy 1222 CGGACCGGCTTGAGC-----GCCGAGAGAGCTTACGCTGGGCGCTATA 1266
Db 1105 CGGAGAGCGCTGTGAAGAGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGTAT 1164
Qy 1267 GTTGTGAGGCTGTGAGAGAGCTGTGAGAGAGATATAGCTGCTACGACTTACGTGAT 1326
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Qy 1327 TACCAAAATCATGATATGATCAATGTGTCTGTACAGCTGTGTGAGGCTGTGTGAA 1386
Db 1225 TACCTCTCATCATCTCCCAACAGCTCTCGCTGATCTCTCAAGAGAGAGTGTG 1284
Qy 1387 AAGTGTGGCGAGTGTGTGTGCGAGGCGCGCGAGAGAGAGAGAGTTCGTAGAGT 1446
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Qy 1447 CGCGCGGCTCTTCAAGAGAGCTGTGAGAGCTGTGAGAGAGAGAGAGTGTAGAG 1506
Db 1333 TTCCAGAGATTTATCCGAGGCTCTCTGAGAGCTCTCTGAGAGAGAGAGAG...GATA 1389
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Db 1450 AAGGCTCATGAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1509
Qy 1627 TGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1686
Db 1510 TGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1569

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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 12:02:29 / Search time 141 Seconds
7550.469 Million cell updates/sec

Title: US-10-034-849-1
Sequence: 1 tagctcgaggtctgtcttcac.....tagccaagaagcagataa 2412

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1119956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : 1 Issued Patents_NA,*
2 /cgn2_6/prodata/1/ina/5b COMB seq.*
3 /cgn2_6/prodata/1/ina/6a COMB seq.*
4 /cgn2_6/prodata/1/ina/6b COMB seq.*
5 /cgn2_6/prodata/1/ina/6c COMB seq.*
6 /cgn2_6/prodata/1/ina/6d COMB seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2412	100.0	2412	2	US-08-907-166-3
2	1063	100.0	2412	4	US-09-181-340-3
3	1045.6	43.3	2430	1	US-08-062-368-1
4	279	11.6	2367	2	US-08-907-166-5
5	19279	11.6	2367	4	US-09-391-340-5
6	162.2	6.7	2337	2	US-08-906-925-5
7	146.2	6.1	2734	1	US-08-375-134-13
8	146.2	6.1	2734	5	US-09-073-358-6
9	131.4	5.4	5339	3	US-09-073-358-6
10	131.4	5.4	5339	3	US-09-363-095-6
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25	110	4.6	3499	1	US-07-966-278-2
26	110	4.6	3499	1	US-07-966-278-2
27	110	4.6	3499	1	US-09-244-889A-2

28 108.4 4.5 2328 4 US-09-715-524B-1 Sequence 1, Appli
29 106 4.4 5837 1 US-07-686-340-1 Sequence 1, Appli
30 106 4.4 5837 1 US-08-004-139B-1 Sequence 1, Appli
31 106 4.4 5837 1 US-08-004-139B-1 Sequence 1, Appli
32 106 4.4 5837 1 US-08-271-364A-1 Sequence 1, Appli
33 106 4.4 5837 2 US-08-811-492-1 Sequence 1, Appli
34 106 4.4 5837 2 US-08-222-715B-1 Sequence 1, Appli
35 102.6 4.1 464976 5 US-08-916-421B-1 Sequence 1, Appli
36 99 4.1 4707 1 US-08-004-139B-2 Sequence 2, Appli
37 99 4.1 4707 2 US-08-811-492-2 Sequence 2, Appli
38 99 4.1 4707 2 US-08-967-1056A-2 Sequence 2, Appli
39 87.4 3.6 2289 4 US-09-391-340-9 Sequence 9, Appli
40 87.4 3.6 2289 4 US-09-391-340-9 Sequence 9, Appli
41 87.4 3.6 2289 4 US-09-391-340-9 Sequence 9, Appli
42 77.6 3.2 2634 4 US-08-907-166-7 Sequence 7, Appli
43 77.6 3.2 2634 4 US-09-391-340-7 Sequence 7, Appli
44 77.6 3.2 2634 4 US-09-391-340-7 Sequence 7, Appli
45 56.2 2.5 1193 1 US-08-239-284A-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-907-166-3 Application US/08907166
; Sequence 3, Application US/08907166
; Matched: 56466
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Mather, Eric
; INVENTOR: Callen, Walter
; FILE REFERENCE: 0910/027001
; CURRENT APPLICATION NUMBER: US/08/907,166
; CURRENT FILING DATE: 1997-08-06
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2412
; ORGANISM: Pyrobolus fumarius
; ORGANISM: Pyrobolus fumarius
; NAME/KEY: CDS
; LOCATION: (1)...(2410)
US-08-907-166-3

Query Match
Best Local Similarity 100.0%; Score 2412; DB 2; Length 2412;
Matches 2412; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

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Db 1 ATGATCGAAGTGTATTACCGGTTTGTAAGTCTAGCTAGCTAGCTGTGTGTAAGAGCT 60
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QY 121 TTTCGCCCAATCTCTGAGGCTGCTGCAAGGCGGCGGCTGCTGAGGAGTACAC 180
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Qy 361. ATACGCTTGGCTATGCTATCTATAGATCAATCTATCTTCTTCACTGATCGCT 420
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Qy 421. CTATAGAGCTGAGCGCTGACAGACAGATAGGCTCTCGGTGTCCAGCATATCTGTTG 480
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Qy 481. ATAGAGCTGAGCGCTGACAGACAGATAGGCTCTCGGTGTCCAGCATATCTGTTG 540
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Db 601. GATCTGTATATATATATATATATATATATATATATATATATATATATATATAT 660
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Db 781. CGCGCATCTATAGCATATAGCATATAGCATATAGCATATAGCATATAGCATATAG 840
Qy 841. AGCGTATATATATATATATATATATATATATATATATATATATATATATATAT 900
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Qy 1021. CCGAGAGATGCGAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCA 1080
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Db 1381. GATATATATATATATATATATATATATATATATATATATATATATATATAT 1440
Qy 1441. ATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500

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RESULT 2
 US-09-391-340-3
 ; Patent No. 6492511
 ; Application US/0939140A
 ; GENERAL INFORMATION:


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Qy 1861 AAGAGAGAGTACGCTGGCTTCTCGAGACCGAGCTATAGATATGTGCGTTTCGAGCT 1920
Db 1861 AAGAGAGAGTACGCTGGCTTCTCGAGACCGAGCTATAGATATGTGCGTTTCGAGCT 1920
Qy 1921 GTATCGGCAATGTGTGATCTCCGACAGAGAGCTCGACTTAAGTGTGTGCAATATGA 1980
Db 1921 GTATCGGCAATGTGTGATCTCCGACAGAGAGCTCGACTTAAGTGTGTGCAATATGA 1980
Qy 1981 TTGAGAGAGAGTGTGACAGAGCTGTAGAGTATGTCAGAGAGATGTGAGAGAGTGTG 2040
Db 1981 TTGAGAGAGAGTGTGACAGAGCTGTAGAGTATGTCAGAGAGATGTGAGAGAGTGTG 2040
Qy 2041 GAGCGAGAGAGTGTGACAGAGCTGTAGAGTATGTCAGAGAGATGTGAGAGAGTGTG 2100
Db 2041 GAGCGAGAGAGTGTGACAGAGCTGTAGAGTATGTCAGAGAGATGTGAGAGAGTGTG 2100
Qy 2101 GAGAGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Db 2101 GAGAGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Qy 2161 TACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Db 2161 TACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
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Db 2221 AGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Qy 2281 TATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
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Qy 2341 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Db 2341 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Qy 2401 AAGAGAGAGTAA 2412
Db 2401 AAGAGAGAGTAA 2412

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RESULT 3

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US-08-062-368-3
/ Sequence 3, Application US/08062368
/ Patent No. 5491086
/ GENERAL INFORMATION:
/ INVENTOR: David H.
/ APPLICANT: Wang, Alice M.
/ CURRENT INVENTION: Polymersases Enzyme From Pyrodicticum Species
/ TITLE OF INVENTION: Purified Thermostable Nucleic Acid
/ ADDRESS: Hoffmann-La Roche Inc.
/ STREET: 340 Kingsland Street
/ CITY: Nutley
/ STATE: New Jersey
/ COUNTRY: U.S.A.
/ ZIP: 07110
/ COMPUTER READABLE FORM:
/ INFORMATION: COPY disk
/ COMMENTS: IBM PC
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 08/06/2003
/ FILING DATE: 08/06/2003
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION: R.
/ REGISTRATION NUMBER: 8584
/ REFERENCE/DOCKET NUMBER: 8584
/ TELECOMMUNICATION INFORMATION:

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/ TELEPHONE: (510) 814-2863
/ TELEFAX: (510) 814-2977
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE LENGTH: 2430
/ LENGTH: 2430 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ COMPOSITION: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-062-368-3

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Query Match: 44.3%; Score 1069.6; DB 1; Length 2430;

Matches 160; Conservative; 0; Mismatches 789; Indels 18; Gaps 4;

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Qy 11 TTGTATTCACGCTTTTACCTTACCTACGAGTGTGTGTAAGAGCCTCAGGTATCA 70
Db 11 TTGTATTCACGCTTTTACCTTACCTACGAGTGTGTGTAAGAGCCTCAGGTATCA 70
Qy 14 TATAGAGTGTGTCTTATAGACTTATCTACAGAGTGTGTGAGAGAGAGAGAGAGT 73
Db 14 TATAGAGTGTGTCTTATAGACTTATCTACAGAGTGTGTGAGAGAGAGAGAGAGT 73
Qy 71 TATGAGAGTATGTCTGAGAGAGAGAGAGAGAGTGTCTTATGACAGGTCTTTTGGCCAT 130
Db 71 TATGAGAGTATGTCTGAGAGAGAGAGAGAGAGTGTCTTATGACAGGTCTTTTGGCCAT 130
Qy 74 TCTGAGAGAGTATGCTTGTGACAGAGAGAGAGTGTCTTATGACAGAGAGAGAGAGT 133
Db 74 TCTGAGAGAGTATGCTTGTGACAGAGAGAGAGTGTCTTATGACAGAGAGAGAGAGT 133
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Db 495 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 547
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Db 545 TACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
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Db 548 TGTAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
Qy 605 CTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 664
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Db 665 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 724
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Db 668 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
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Db 848 TCTACGCCACCTCTCGTGTGAGGTAGGCTGACGTGACCTCTAGACTATGCGAGG 907
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 Db 908 AGATTCACAGATCAAGATGATCTCGAGAGGTGCTGAGAGTATCTTAGGGTGTGTA 967
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 Qy 1025 AGAGAGACACATATATCTCATATGTTGGTGGAGATCTCGAGATCTTAGGGAGCCGA 1084
 Db 1028 AGAGAGACACATATATCTCATATGTTGGTGGAGATCTCGAGATCTTAGGGAGCCGA 1087
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 Db 1088 CCGAGAGATATATGCTTTGCTATCCAGTGTGTGTAAGACAGTCTTCCAGCTAGAC 1147
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 Db 1685 GCAAGCTCTGCGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCA 1747
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 Db 1745 GCTGCTCTGCGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCA 1807
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 Db 1805 AGCTGCTCTGCGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCA 1867
 Qy 1862 AGAGAGTCTGCGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCA 1921
 Db 1865 AGAGAGTCTGCGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCA 1927
 Qy 1922 TAGCTGCTCTGCGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCA 1981
 Db 1925 TAGCTGCTCTGCGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCAAGAGGAGTCTTCA 1987

Qy 1982 TGAAGAGAGTGAAGTGAAGAGCTGTAGAATAGTCTGAGAGATGTGTGAAGAGTGTG 2041
 Db 1985 TGAAGAGAGTGAAGTGAAGAGCTGTAGAATAGTCTGAGAGATGTGTGAAGAGTGTG 2047
 Qy 2042 AGAGAGAGT 2101
 Db 2045 AGAGAGAGT 2107
 Qy 2102 AGAGAGT 2161
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 Qy 2162 AGAGAGT 2221
 Db 2165 AGAGAGT 2227
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 Db 2225 GTCAAGAGAGT 2284
 Qy 2282 GTCAAGAGAGT 2341
 Db 2285 GTCAAGAGAGT 2344
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 Db 2345 AGAGAGAGT 2404
 Qy 2402 AGAGAGAGT 2459
 Db 2405 AGAGAGAGT 2462

RESULT 4 US 05-034-368-1

; Sequence 1, Application US/08062368
 ; Patent No. 5491086
 ; GENERAL INFORMATION:
 ; APPLICANT: Galand, David H.
 ; TITLE OF INVENTION: Purified Thermostable Nucleic Acid
 ; NUMBER OF SEQUENCES: 35
 ; COMPLETION DATE: 1997
 ; ADDRESS: Hoffmann-La Roche Inc.
 ; STREET: 340 Kingland Street
 ; CITY: Nutley
 ; STATE: New Jersey
 ; COUNTRY: U.S.A.
 ; ZIP: 07110
 ; COMPUTER READABLE FORM:
 ; FILE TYPE: ASCII
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 19930514
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Size Ph. D., Stacey R.
 ; ADDRESS: 2400 N. 1st St., Suite 200, Newark, NJ 07102-4584
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 814-2863
 ; FAX: (610) 814-2863
 ; INFORMATION FOR SEQ ID NO. 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2430 base pairs
 ; TYPE: nucleic acid
 ; STRATEGY: full length
 ; TOPOLOGY: linear

Db 1826 ATGAGAGATTAATGTAAGGGCTTGAAGTCAGAGAGCGCACTGGTGAGCTGCA 1885
 Qy 1949 AGAGAGTTCAGATCAGAGTGTGCAATATGATTAAGAGCGAGTGAGTGAACAGGGCTG 2008
 Db 1886 AGAGATTAAGAGTGTATAGATTAATGATTAATGATTAATGATTAATGATTAATG 1945
 Qy 2008 TAGAGTACCTCAGAGAGATTTGAGAGGTGTGAGAGGTGAGAGGTGAGAGGTGAGAG 2068
 Db 1946 TAGAGTGTGAGAGAGCTCAGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGT 2005
 Qy 2069 TGTATATTCAGAGAGCTTGTAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGT 2128
 Db 2006 ATATCTATTCAGAGAGCTTGTAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGT 2065
 Qy 2129 TGTGTGTGAGAGAGCTTGTAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGT 2188
 Db 2066 TTAGAGTGTGAGAGAGCTTGTAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGT 2125
 Qy 2189 GTATATTCAGAGAGCTTGTAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGT 2248
 Db 2126 GTTTGTGCTTACAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGTGTGAGAGGT 2185
 Qy 2249 TCAAGGA 2255
 Db 2186 TAGAGA 2192

RESULT 6

US-09-391-340-5
 ; Patent No. 6492511
 ; GENERAL INFORMATION:
 ; APPLICANT: Callen, Walter
 ; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF NOVEL POLYMERASES
 ; FILE REFERENCE: 09010/027001
 ; CURRENT APPLICATION NUMBER: US/09/391,340A
 ; EARLIER APPLICATION NUMBER: 06/507,166
 ; EARLIER FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 12
 ; SEQ ID NO 5
 ; LENGTH: 2367
 ; TYPE: DNA
 ; ORGANISM: Archaeoglobus lithotrophicus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(2364)
 US-09-391-340-5

Query Match 11.6%; Score 279; DB 4; Length 2367;

Best Local Similarity 50.9%; Pred. No. 5,1e-79;

Matches 889; Conservative 0; Mismatches 795; Indels 63; Gaps 7;

Qy 530 TTTCGGCTTTCAGAGTACTGCTGCTGATTAAGTTATAGCAAGAGGTGGCGC 589
 Db 488 TTTCGGCTTTCAGAGTACTGCTGCTGATTAAGTTATAGCAAGAGGTGGCGC 547
 Qy 590 GTCCAGAGCGGCTCTGATTAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 649
 Db 548 GTCCAGAGCGGCTCTGATTAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 607
 Qy 650 TATTCATTCAGAGAGGCTGATTAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 709
 Db 608 TATTCATTCAGAGAGGCTGATTAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 658
 Qy 710 AGAGTATTCAGAGAGGCTGATTAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 769
 Db 659 GCGATATTCAGAGAGGCTGATTAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 718
 Qy 770 TTTCGGCTTTCAGAGTACTGCTGCTGATTAAGTTATAGCAAGAGGTGGCGC 829

Db 719 TCAGAGAGAGCTGAGAACTGAGGGTTAAGCTTGACATCGAGAGATTAAGAGCGAAC 778
 Qy 830 AGCCGCCATCTAGCTACATGAGGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 889
 Db 779 TGTCTTCTGAGGAG 832
 Qy 890 AGCAGTATTCGAGAGAGATTCGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 949
 Db 833 ATATCTATTCGAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 892
 Qy 950 ATATCTATTCGAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 1009
 Db 893 TTCTGAGTAAAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 952
 Qy 1010 ATATGAG 1069
 Db 953 CATCGGCGAG 1003
 Qy 1070 CTATCTAGAGAGTCTGAG 1129
 Db 1004 ACAAGTCTATTCAG 1063
 Qy 1130 GTCT 1189
 Db 1064 GCATCT 1123
 Qy 1190 TACAGCGGAGTCTGAG 1249
 Db 1134 TACAG 1180
 Qy 1250 CTATCTAG 1309
 Db 1181 GCTATCTAG 1240
 Qy 1310 TCGAGTCTGAG 1369
 Db 1241 TCGAGTCTGAG 1300
 Qy 1370 TTGTGAG 1429
 Db 1301 TTGTGAG 1348
 Qy 1430 ACAGTCTGAG 1489
 Db 1349 ACAGTCTGAG 1408
 Qy 1490 TTCTGAG 1549
 Db 1409 AAG 1468
 Qy 1550 TTGTGAG 1609
 Db 1469 TGTCTATATTAAG 1528
 Qy 1610 GTTGGAG 1669
 Db 1523 GTTGGAG 1588
 Qy 1670 GCGAGTCTGAG 1729
 Db 1589 GAGATCTATTAAG 1748
 Qy 1730 GTTGGAG 1789
 Db 1649 GCGATATTCAG 1708
 Qy 1790 TATTAAG 1828
 Db 1709 AAGTATTAAG 1768
 Qy 1829 AGAGTATTAAG 1888
 Db 1769 ATATCTAG 1825

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1889 ACGAGGTATAGATATTGCGGTTTCAGCGTGTACGTGCGATGTTGTGTAATCGCCA 1948
1948 ATAGAGAGATTAATTGTAAAGGCGTTTGAGGTACAGAGAGAGCGATGTTGCGACTTCGA 1885
1949 AGAGGTTGCGAGTTCAGGTTGTGTAATGATATGAGACAGATGAGGTGACAGGCTG 2008
1949 ATGAGGTTGCGAGTTCAGGTTGTGTAATGATATGAGACAGATGAGGTGACAGGCTG 2008
1886 AGAGATACAGAGAGGTTGTAATGAAATGATCTTGAGAGAAAGATATCTGAAAAGCTG 1945
2003 TGAGTACTCCGAGAGATGTTGTAATGAGATGTCAGAGTTCGAGGCTCCCTTACAGACC 2068
1946 CTGATGATGTGAAGAGGCTGTAGAGAGATTAAGAGCGAGCAAAATTCGCTTGAGATT 2005
2065 TGTATGTTGCGAGAGGCTGTGTAAGGCTGTGAGAGATGTCAGAGGCTGCGACAG 2128
2066 ATATGATCTACAGAGATGACAGAGAAACATCAAGTACAGAGATGTCAGAGCTCAG 2065
2129 TCGTTCGCGAGAGAGGCTGTCAGAGGCTCAGGCTGAGCCGAGAGAGAGATG 2188
2066 TAAAGGCTGCTGAGAGGCGAAGAGAGAGATGATATACATGCTGCAAGGCTG 2125
2189 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2248
2126 GTTGTGTGTGTAAGAAGGTGTGAGAGATGATGATGATGATGATGATGATGATGATG 2185
2249 TCAAGA 2255
2186 TAGAGA 2192

RESULT 7
US-08-902-632-3
; Sequence 3, Application US/08902632
; Patent No. 6068025
; GENERAL INFORMATION
; APPLICANT: KITAABAYASHI, Hideyuki
; APPLICANT: KITAABAYASHI, Masao
; APPLICANT: KAMIMURA, Hideki
; APPLICANT: KAWAMORI, Bunsei
; APPLICANT: KAWAMORI, Masahiro
; APPLICANT: TANAGI, Masahiro
; APPLICANT: IMANAKA, Tadayuki
; TITLE OF INVENTION: Modified Thermostable DNA Polymerase,
; TITLE OF INVENTION: Modified Thermostable DNA Polymerase,
; TITLE OF INVENTION: Modified Thermostable DNA Polymerase
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; INVENTOR: Kitayoshi, Masao & Kenyon
; STREET: 1 Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch floppy disk, 1.44 Mb storage
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: PowerPerfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,632
; APPLICATION DATE: 30-JUL-1996
; CLASSIFICATION: 415
; PRIORITY INFORMATION:
; APPLICATION NUMBER: JP 198911/96
; APPLICATION DATE: 30-JUL-96
; APPLICATION NUMBER: JP 200446/96
; APPLICATION DATE: 30-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CREASON, Edward W.
; FIRM: CREASON, Edward W.
; REFERENCE/DOCKET NUMBER: 2418/7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-425-7200

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; TERMID: 212-425-5288
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; US-08-902-632-3

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Query Match 7.91; Score 191.4; DB 3; Length 2325;
Beac Local Similarity 48.01; Pred. No. 3,4e-50;
Matches 854; Conservative 0; Mismatches 856; Indels 69; Gaps 8;
QY 622 GTGAGAGCTGACGAGTGTGAGGCTGATCTATCATGTCAGAGGCGAAGACGATCGA 681
Db 508 GTGAGAGCTGACGAGTGTGAGGCTGATCTATCATGTCAGAGGCGAAGACGATCGA 567
QY 682 CGGATGAGGCTGATGAGTGTGAGGCTGATCTATCATGTCAGAGGCGAAGACGATCGA 741
Db 568 ATATGAAAGGCTTCTCCGTTGTGAGAGAAACCGGAGCTTCTCATTAACCTAC 627
QY 742 AACGACATCATTTGATGCGCTTACTTTTATGCGCGCCGCGGCTGCTGAGCGAAG 801
Db 801 AACGACATCATTTGATGCGCTTACTTTTATGCGCGCCGCGGCTGCTGAGCGAAG 801
QY 628 AACGCGCAACCTGATCTCCGCTTACTTATAAAGAGCGCTGTGAAGCTTCGATTAAC 687
Db 802 CTGTATGATGATGAGAGGCTTTCGAGCGCCGCGGCTGATGATGATGATGATGATGATG 861
QY 688 TTGCGCTCGAGAGCGATGAGAGCGAGCGAGAGCGAGAGCGAGAGCGAGAGCGAGAG 747
Db 921 GTCTCTGCGAGCTTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 921
QY 748 GTTGAAGTGAAGAGCGGATACCTGATCTTATCTTGATTAAGAAGAGAGATTAAC 807
Db 922 ATAAAGATCTCGAGAGGCTGCGAGGCTGATGATGATGATGATGATGATGATGATGATG 981
QY 808 CTGCCCAATACAGCTGTAGCGCTGATGATGATGATGATGATGATGATGATGATGATG 864
Db 982 ATCATCATTTGAGAGCTTCGAGCTTATGAGCGATGATGATGATGATGATGATGATGATG 1041
QY 865 TATGCGTGTGAGTAAATTAACAGAGCTGAGAGAGCGAGAGAGAGAGAGAGAGAGAG 924
Db 1042 CTGCAATCTGAGAGAGCTGCGGCTGCTTACGCTTACGCGAGAGAGATATACCG 1101
QY 925 GCGCGCTATCATGATGAGATGAGAGGCTGATGAGAGGCTGATGAGAGGCTGATGAG 984
Db 1102 TTGTCTATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1161
QY 985 ATGAGAGCGAGCTTTGCTTTATGTCGATGATGATGATGATGATGATGATGATGATG 1044
Db 1162 GTTGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1221
QY 1045 ACTGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1104
Db 1222 CGAGACGCGGTGTAGC-----GCCGAGAGAGATTTACGTCGCGGTATA 1266
QY 1105 CGAGAGAGCGCGGTGTAGC-----GCCGAGAGAGATTTACGTCGCGGTATA 1164
Db 1267 GTTCTTGTGAGGCTGTGAGAGGCTGCGAGAGATTAAGCGCTACTGAGCTTTAGCTGATG 1326
QY 1155 GTAAAGAGCGCGGTGTGAGAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1224
Db 1327 TATCCCAAGATCATGTAAGATCAATGTGCTGACACCTCTGAGAGGCTGAGAGAGAG 1386
QY 1225 TACCTCTCATATCATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1284
Db 1387 AAGTGTGCGAGGTGTGCTGCGAGAGCGCGCGAGGCTCAAGCGAGGTTCGATGAGTGT 1446
QY 1285 AAGTGTGAGTGTGCTT-----GCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1332
Db 1447 CGCGCGGCTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1506
QY 1333 TTCCAGAGATTTATCCCGAGAGCTGCTTGAAGAGCTTCTTGAAGAGAGAGAGAGAGAG 1389

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Oy 983 TCATCATCTGTTGGAGGATTCAGACTATTCGGACAGCCGAGAGAGACACTATAC 1042
Db 986 AGGCTATGACCGAGAGATGACACACCTCTGGAGACACCGAGAGGGGCTTGAGAGGGTGG 925
Oy 1043 TGCATATAGCGCGAGCATGATGTCGGGCTACTTACAGGCTTACCCGAGAGATATTCGGCT 1102
Db 926 GCGGCTATCTGATGAGAGAGCGAGAGGGGTATCTATGAGCTTGGAGAGAGATTTCTCCGA 985
Oy 1103 TGGCTATATCAGATGAGAGAGCGAGGGGTCTCCGATAGACAGCTTACCGCTATGATGATG 1162
Db 986 TGAAGCGCGAGCTTTCAGGCTCATCTGGCAGAGGTCTCTGGAGAGCTTTCCGCTCGACA 1045
Oy 1163 TTGGCTTTGCGATCTGAGATGATCTGATGAGCGCGGGGTTTATGATTAAGAGAGTGTGCG 1222
Db 1045 CCGGGAAGCTTTGATGATGATTTTCTCTGAGAGAACTTACAGAGAGAGCACTGCTC 1105
Oy 1223 GAGAC-----CGGTGTAGCTTCCGAGAGAGCACTTACCGGTGGGCTATAG 1267
Db 1106 CAGAGAGCCGAGAGAGAGAGAGCTGCGAGAGATATAGCGGTACTTACGATTTAGCTGAT 1165
Oy 1268 TTCTTGAAGCTGTGAGAGAGCGTGCAGAGATATAGCGGTACTTACGATTTAGCTGATGAT 1327
Db 1166 TGAAGAGAGTGGAGAGAGCTGAGAGATATATATGATGATCTGATTTTCTGCTGCTGT 1245
Oy 1328 ACCGAAATCATATATATATGATATGATGTTCTGAGAGAGCTTGTGAGGCTCGGTGAA 1387
Db 1226 ACCGCTTATATATATCCGAGAGCTTCTGCGATGCTGATGCTGATCCGAGAGAGATGTA 1285
Oy 1388 AGTGTGAGATGATGATGTTGCTGGAGAGCCCGAGAGCTCAAGACAGGTTCGGATGATGTC 1447
Db 1286 AGAGCTAGAGCTT-----GCCCCGAGAGGTGTCTGAGAGTCTGCAAGCT 1393
Oy 1448 GCGCGGCTTCTTCAGACAGTCTTGAAGAGCTGTAGAGCTTGTGATAGGTGTGGTG 1507
Db 1334 TCCCGGCTTCATTCGAGAGCTTCTGAGATGCGGAACTCTCGAGAGAGCGAGAGTAAGA 1393
Oy 1508 CTGAATGAGAGATATCTTCGATAGCCGAGAGATATGATCTGATGATGAGAGCGA 1567
Db 1394 GAGAGATGAGGC--AAAGCTCGACCGCTGGAGAGAGCTTCTGATATATGCGACG 1450
Oy 1568 AGGCTGATGAGCTTCTGAGAGAGTATGAGCTTACGCTGAGAGAGAGCTTCTGATATGCGAGT 1627
Db 1451 GGCCTATCAAAATCTGAGAGAGCTTCTGAGAGCTTATACGCTAGCGAGAGAGAGAT 1510
Oy 1628 GTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1687
Db 1511 GATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1570
Oy 1688 CAGCA--KAGAGCTGTAACTAGCTTGAAGATATTAAGATATTAAGAGAGAGAGAGAGAG 1744
Db 1571 TTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1630
Oy 1745 TCTGAGAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1802
Db 1631 TTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1690
Oy 1803 -----GCTGGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1691 TTAACATATATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1750
Oy 1841 GCTATTTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1900
Db 1751 TCTGGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1810
Oy 1901 ATATTTGCTGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1960
Db 1811 CAGCGCGGCTTGAAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1870
Oy 1961 CTAGAGTGTTCGAATAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2020
Db 1971 CAGAGGTTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1930
Oy 2021 GGAAGATTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2080

```

RESULT 9

US-08-375-134-13

Sequences 13 Application US/08/375134

Sequences 13 Application US/08/375134

GENERAL INFORMATION:

APPLICANT: Luhm, Robert A.

APPLICANT: d'Hemmel, Olga B.

APPLICANT: d'Hemmel, Olga B.

APPLICANT: Kelly, Robert M.

APPLICANT: Ting, Yve Yi-Fay

INVENTOR: PURIFIED THERMOCCOCUS BAROSSII DNAPOLYMERASE

NUMBER OF INVENTION: 3

CORRESPONDENCE ADDRESS:

ADDRESS: Quarles & Brady

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: WISCONSIN

COUNTRY: U.S.A.

ZIP: 53202-4497

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/375,134

FILING DATE:

CLASSIFICATION: 435

ATMOSPHERE/AGENT INFORMATION:

NAME: Robert A. Luhm

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 740211.90440

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 271-3570/9

TELEFAX: (414) 271-3570/9

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 2734 base pairs

STRANDS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-375-134-13

Query Match 6.11; Score 146.21; DB.1; Length 2734;

Best Local Similarity 45.21; Pred. No. 8.7e-36;

Matches 884; Conservative 0; Mismatches 1008; Indels 63; Gaps 7;

1 ADDRESS: Quarles & Brady
2 STREET: All East Wisconsin Avenue
3 CITY: Milwaukee
4 STATE: WISCONSIN
5 COUNTRY: U.S.A.
6 ZIP: 53202-1497
7 CIP: 53202-1497
8 CIP: 53202-1497
9 CIP: 53202-1497
10 CIP: 53202-1497
11 CIP: 53202-1497
12 CIP: 53202-1497
13 CIP: 53202-1497
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100 CIP: 53202-1497

Query Watch	Score 146.21	DB.5	Length 2734
Best Local Similarity	45.21	Prod. No. 8.7e36	
Matches 843	Conservative 0	Mismatches 1008	Indels 63
Gaps 71			
Qy	44	ACAGATCGGCTTCGGTGTCCGACGAGTCTGTTTAAAGCGCGCGGAGCATT	502
Db	565	ACGAGTAGCAATACCTTCGACAGGCTATCTCATAGAGAGGCTTGATCTCAAG	624
Qy	503	ATGTGAGGCTTCGCAACACAAAGCTCCGAGTCTAGAGATATCCGGTTCGATTG	562
Db	625	AGGCGCTATCGGAGCTTATACCTATGTCTTCGATCGAGAGCTCTACACGAGGAG	684
Qy	563	AGGTTTATAGCAAGCAAGGTCGCGCTCGACAGCGCATCTGTATATGATGACTG	622
Db	685	ATAGATTCGAGACCGGCGCAATCTGATATAGCTATACGCGGTGAAGCGAGGCGGTG	744
Qy	632	TGAAGTTCGAGCGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	682
Db	745	TGATTAATCTGGAAGATCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	804
Qy	683	CGATTCGGAGCTTTTATGCTACTGAGAGGATATATCCCGACATATATGTGGTTAT	742
Db	805	TGATTAAGCGCTTCTTATAGTCTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	864
Qy	743	ACACCAATCTTCGATCGGCTTATCTTTTATGAGCGCGCGCGCATCTTAGCATTAAGC	802
Db	865	ACGATCTTATGAGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT	924
Qy	803	TTGATGTGCTATGAAGTCTCGCGCGAGCCACATGACTGACTGAGCACTGCTCTG	862
Db	925	TACCTCTCGCGAGAGCGGCGAGCGAGAGATACAGCGGAGAGGCGAGCGCTTCCCG	984
Qy	863	TCCGTCGAGGCTTAAGTGAATCTGTGTGATCTTGTGCGAAGATATCCGAGATCTAG	922
Db	985	TGAGTGAAGAGGAGAGATCCACTTGCATCTGATCCCGTATGCGGCGACCATTAAC	1044
Qy	923	TATAGAGTCTCGAGAGGCTCGAGATCTTATAGGCGGTGTGAAGAGATGAGACCGTTA	982
Db	1045	TTCGCACTAGCTATGAGTCTTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1101
Qy	983	TCATCATGTGTGGAGATTCGACAGCTTTGGGAGAGAGCGCCGAGAGAGAGCATATTAC	1042

[illegible]


```

1 APPLICANT: KAWAKURA, Yoshiyasu
2 APPLICANT: INAMURA, Tadakuji
3 APPLICANT: TANAKA, Masahiro
4 APPLICANT: MORIKAWA, Masaaki
5 TITLE OF INVENTION: A Method of Amplifying Nucleic Acids by Polymerase Chain Reaction and a Reagent Therefor
6 NUMBER OF SEQUENCES: 16
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Kenyon & Kenyon
9 ATTORNEY/AGENT INFORMATION: Kenyon & Kenyon, 100 Connecticut Avenue, N.W., Suite 600
10 CITY: Washington
11 STATE: D.C.
12 COUNTRY: USA
13 COMPUTER RELEASABLE FORM:
14 MEDIUM TYPE: 3.5" Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 CURRENT APPLICATION OR PRIORITY REFERENCE: 5.1
18 APPLICATION NUMBER: US/08/656,005A
19 FILING DATE: 24 May 1996
20 CLASSIFICATION: 435
21 PATENT OFFICE ACTION DATA:
22 APPLICATION NO.: DRA
23 FILING DATE: 31 MAY 1995
24 ATTORNEY/AGENT INFORMATION: NAME: Yofumetsu, Judith L.
25 REFERENCE/DOCKET NUMBER: 95-091819/3
26 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-423-1776
27 FAX/FAX: 202-423-0796
28 INQUIRY CONTACT PERSONS: 6
29 SEQUENCE CHARACTERISTICS: LENGTH: 5339 base pairs
30 TYPE: nucleic acid
31 ORGANISMES: double stranded DNA
32 TOPOLOGY: linear
33 MOLECULE TYPE: cDNA
34 ORIGINAL SOURCE: Hypothermophilic archaeon
35 US-08-656-005A-6
36 Query Match 5.4%; Score 131.4; DB 3; Le
37 Best Local Similarity $2.2%; Pred.No. 6.7e-31;
38 Matches 4192; Conservative 0; Mismatches 341; In
QV 1597 TAGCGTCACAGTGGTTGACGCATCCGTCTCATGCAAGGCGCGTGACTCCTCGAAC
DB 4320 TACGGATTACAGCGCTCATGAAGCGGCGCGTGACTCCTCGAAC
QV 1657 AGCGCTCGGGGTAGCGACTCTTATGCCACGCGCACAC-C-A
DB 4380 ACCCGCTGGGAGAGAGTAGTACATAAGGAGACATCGACATCGAGA
QV 1714 TCAGAGGTATATCGNGNAGACAGGATTCGCTCTCGAGCT
DB 4440 TTTAAGSTATACAGACACAGCGGATTTTCCTCAA
QV 1774 GAAATTTTCATAAAATATAAAGAGAGAGCTG-----
DB 4500 GAAACGCTAAAAGAGAGCTCTAGAGATTTCTCAACTATATCA
QV 1807 GGATTTCGAATCAAGCTACAAGAGGGTTGTACACAGCGTTATCT
DB 4560 CGGCTCGGCTTCTGACGAGAGCGGATTTTCCTCAA
QV 1867 AGGTATCGTGGCTCTGTCTGACAGAGAGAGGATATAGATATATGCG
DB 4617 ATATTCGCGATATACACGAGAGAGAGAGATACACACGCGG
QV 1927 GCAGATTTGGTGTACTGCTCCAGAGAGGTTCTGACAGGCT

```

STRANDNESS: double
 TITLE OR INVENTION: RNA Encoding A Thermostable RNA Polymerase
 MOLECULE TYPE: RNA
 ORIGINAL SOURCE: Hyperthermophilic archaeon

US-09-363-259-6

Query Match 5.4%; Score 131.4; DB 3; Length 5339;
 Best Local Similarity 52.2%; Pred. No. 6.7e-31;
 Matches 412; Conservative 0; Mismatches 341; Indels 36; Gaps 4;
 QY 1597 TAGCGTCACTAGTGTGGACGGCGCGTATGTTATTCGAGAGTGCCTCAAGCGTCTC 1656
 DB 4320 TACGCTTACAGCGTATGCGACGGCGCGTCTGCTATCTACAGAGTGTCTGAGAGCTA 4379
 QY 1657 AGCGTCTGGGATGAGCACTCTATGACGACCGCCATCACC---ATAGCTGTAACTAGCG 1713
 DB 4380 AGCGTCTGGGATGAGCACTCTATGACGACCGCCATCACC---ATAGCTGTAACTAGCG 4439
 QY 1714 CTCAAGGCTATGATCAGGAGTGCACAGATTCGCTCTGTGAGCTATGATCCGAGAGGTG 1773
 DB 4440 TTTAAGGTATCTACGACGCTATGAGCGAGTCTTTTCCGATCTCTGAGCCGCTCT 4499
 QY 1774 GAAATTTCTCAAAATATATAAGAGGAGCTG-----1806
 DB 4500 GAAACGCTCAAAAGAGCTATGAGTCTCACTATATCAAGCGAACTTCGCGGC 4559
 QY 1807 GGGTGTGAAATCAAGCTAGAGAGGTTCACAACTTATTTTACAGAGGCTAAAG 1866
 DB 4560 GCGCTGTAGCTCGAGTACGCGGCTCTTCAACAGCGCTCTT---CGTCAGAGAG 4616
 QY 1867 AGTGAAGCTGCGCTCTCTCGAGCGAGCTATGATATGTGCTTTCGAGGCTGTAGCT 1926
 DB 4617 AGTGAAGCTGCGCTCTCTCGAGCGAGCTATGATATGTGCTTTCGAGGCTGTAGCT 4676
 QY 1927 GCGAGTGTGTGAGCTCGCAGAGAGTTCAGCTAGAGTGTGCAATAGTATTCGAG 1986
 DB 4677 GGTGATGAGCGAGTATGCGAAGAGAGCGCGAGGAGTCTTGAAGCTTGTGAG 4736
 QY 1987 ACGAGTGAAGTGAAGCGGTAGAGTACTCAGAGAGTGTGAGAGTGTGAGAGTTCGAG 2046
 DB 4737 GAGTGAAGTGTCCATAGAGAGGCTGTATCTGGAAGAGCTTACGAAAGCTTAGAG 4796
 QY 4797 TAGAGGATTTCCCGCGCAAGAGCTGTGATCTCAGCGCGAGTAAAGAGTAAAGAG 4856
 QY 2107 TACACAGCGAGCGACGCTGTGCTGTGAGCGAGAGGCTGTCTGACGCTCAAG 2166
 DB 4857 TAAAGGCGACAGCGCTCCCACTGTTTCCGCTTCCAGAGTGTGCGCGAGAGGTCAA 4916
 QY 2167 GTAAGCGCTGCGAGCTAGAGTGTATATGAGAGTGTGCGCGAGTGTGCGCGATCAA 2226
 DB 4917 ATACGCTCTGGAAGCGGTATAGCTATCATCTGCTCAAGGCTCTGAGGATGAG 4976
 QY 2227 AGAGATGCGCTACTTCTATGCTGAGAGATCTATGCGATAGTGTGAGCT---TACTAT 2283
 DB 4977 AGGCGATACGCTTCAGAGTTCGACCGCGAGCGAGCTAGCTAGCTGAGTATGAG 5036
 QY 2284 GTTACGACCAATATCTCCGCGATATGAGATATCTGCGCTACTTGTGCGATCAAGG 2343
 DB 5037 ATTAGAGCAAGGCTCTCCGAGCGCTGAGAGAGTCTTGAAGAGCTCTGTTTACCG 5096
 QY 2344 AAGAAAGCTG 2352
 DB 5097 GAGAGAGCTG 5105

RESULT 14

US-09-363-259-6
 Sequence 6, Application US/09363095
 Patent No. 6187573
 GENERAL INFORMATION:
 APPLICANT: IMVUNA, Tadayuki

APPLICANT: TAKAGI, Masahito
 APPLICANT: MORTKAWA, Masaki
 TITLE OR INVENTION: RNA Encoding A Thermostable RNA Polymerase
 MOLECULE TYPE: RNA
 ORIGINAL SOURCE: Hyperthermophilic archaeon
 CURRENT APPLICATION NUMBER: US/09/363,095
 EARLIER FILING DATE: 1999-07-30
 EARLIER APPLICATION NUMBER: US/09/073,259
 EARLIER FILING DATE: 1999-07-30
 EARLIER APPLICATION NUMBER: US/09/656,005
 EARLIER FILING DATE: 1996-05-24
 EARLIER APPLICATION NUMBER: JP 134096/95
 EARLIER FILING DATE: 1995-05-31
 NUMBER OF SEQ. IDS: 6
 SOFTWARE: WordPerfect 6.1 Windows
 SEQ ID NO 6
 LENGTH: 5339
 ORGANISM: Hyperthermophilic archaeon
 FEATURE:
 OTHER INFORMATION:
 US-09-363-095-6

Query Match 5.4%; Score 131.4; DB 3; Length 5339;
 Best Local Similarity 52.2%; Pred. No. 6.7e-31;
 Matches 412; Conservative 0; Mismatches 341; Indels 36; Gaps 4;
 QY 1597 TAGCGTCACTAGTGTGGACGGCGCTGATGTTATTCGAGAGTGCCTCAAGCGTCTC 1656
 DB 4320 TACGCTTACAGCGTATGCGACGGCGCGTCTGCTATCTACAGAGTGTCTGAGAGCTA 4379
 QY 1657 AGCGTCTGGGATGAGCACTCTATGACGACCGCCATCACC---ATAGCTGTAACTAGCG 1713
 DB 4380 AGCGTCTGGGATGAGCACTCTATGACGACCGCCATCACC---ATAGCTGTAACTAGCG 4439
 QY 1714 CTCAAGGCTATGATCAGGAGTGCACAGATTCGCTCTGTGAGCTATGATCCGAGAGGTG 1773
 DB 4440 TTTAAGGTATCTACGACGCTATGAGCGAGTCTTTTCCGATCTCTGAGCCGCTCT 4499
 QY 1774 GAAATTTCTCAAAATATATAAGAGGAGCTG-----1806
 DB 4500 GAAACGCTCAAAAGAGCTATGAGTCTCACTATATCAAGCGAACTTCGCGGC 4559
 QY 1807 GGGTGTGAAATCAAGCTAGAGAGGTTCACAACTTATTTTACAGAGGCTAAAG 1866
 DB 4560 GCGCTGTAGCTCGAGTACGCGGCTCTTCAACAGCGCTCTT---CGTCAGAGAG 4616
 QY 1867 AGTGAAGCTGCGCTCTCTCGAGCGAGCTATGATATGTGCTTTCGAGGCTGTAGCT 1926
 DB 4617 AGTGAAGCTGCGCTCTCTCGAGCGAGCTATGATATGTGCTTTCGAGGCTGTAGCT 4676
 QY 1927 GCGAGTGTGTGAGCTCGCAGAGAGTTCAGCTAGAGTGTGCAATAGTATTCGAG 1986
 DB 4677 GGTGATGAGCGAGTATGCGAAGAGAGCGCGAGGAGTCTTGAAGCTTGTGAG 4736
 QY 1987 ACGAGTGAAGTGAAGCGGTAGAGTACTCAGAGAGTGTGAGAGTGTGAGAGTTCGAG 2046
 DB 4737 GAGTGAAGTGTCCATAGAGAGGCTGTATCTGGAAGAGCTTACGAAAGCTTAGAG 4796
 QY 2047 GGCAGAGTTCGATAGAGAGCTGTATCTCGAGAGCGCTTATGTAGAGCTCTGAGGAG 2106
 DB 4797 TACGAGTCTGCGCGAGAGCTGTGATCTCAGAGAGCTTACGAGGAGTAAAGAGC 4856
 QY 2107 TACACAGCGAGCGACGCTGTGCTGTGAGCGAGAGGCTGTCTGACGCTCAAG 2166
 DB 4857 TAAAGGCGACAGCGCTCCCACTGTTTCCGCTTCCAGAGTGTGCGCGAGAGGTCAA 4916
 QY 2167 GTAAGCGCTGCGAGCTAGAGTGTATATGAGAGTGTGCGCGAGTGTGCGCGATCAA 2226
 DB 4917 ATACGCTCTGGAAGCGGTATAGCTATCATCTGCTCAAGGCTCTGAGGATGAG 4976
 QY 2227 AGAGATGCGCTACTTCTATGCTGAGAGATCTATGCGATAGTGTGAGCT---TACTAT 2283
 DB 4977 AGGCGATACGCTTCAGAGTTCGACCGCGAGCGAGCTAGCTAGCTGAGTATGAG 5036

Qy 2284 GTTACACCAATATCCCGCTGATATGATGATCTGGGTACTTGTGCATCCAG 2343
 Db |||||
 Qy 5037 ATTGAGACAGAGCTCTCCAGCCCTTGAGAGAGATCTGAGAGGCTCTGTTACCGGAG 5096
 Qy 2344 AGAAGACT 2352
 Db |||||

Qy 5097 GAGAGCTG 5105

RESULT 15

US-09-418-027-6 Application US/09418027
 Patent No. 6235065
 GENERAL INFORMATION:
 APPLICANT: KITABAYASHI, Masao
 APPLICANT: KITABAYASHI, Masao
 APPLICANT: INOUE, Hiroaki
 APPLICANT: KANAKAMI, Bunsei
 APPLICANT: KANAKAMI, Yoshihisa
 APPLICANT: KANAKAMI, Yoshihisa
 APPLICANT: KANAKAMI, Tadayuki
 APPLICANT: KANAKAMI, Tadayuki
 APPLICANT: MORIYAMA, Masaki
 APPLICANT: MORIYAMA, Masaki
 TITLE OF INVENTION: A Thermostable DNA Polymerase and Kits for
 TITLE OF INVENTION: Amplifying Nucleic Acids
 TITLE OF INVENTION: Amplifying Nucleic Acids
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenyon & Kenyon
 STREET: 1025 Connecticut Avenue, N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20036

COMPUTER READABLE FORM:
 FILE: US-09-418-027-6.FLIPPY.DISK
 COMPUTER: IBM PC
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 6.1 Windows
 CURRENT APPLICATION DATA:
 FILING DATE: 09/09/1997
 PRIORITY DATE: 09/09/1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: 09/073,354
 FILING DATE:
 APPLICATION NUMBER: JP 134096/95
 FILING DATE: 31 MAY 1995
 NAME/AGENT INFORMATION:
 NAME/AGENT INFORMATION: L.
 REGISTRATION NUMBER: 39,048
 REFERENCE/DOCKET NUMBER: 2418/9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-424-0726
 TELEFAX: 202-424-0726
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5339 base pairs
 TYPE: nucleotide
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORGANISM: SOURCE: Hyperthermophilic archaeon

US-09-418-027-6
 Query Match 5.4%; Score 131.4; DB 3; Length 5339;
 Best Local Similarity 52.2%; Pred. No. 6.7e-31;
 Matches 412; Conservative 0; Mismatches 341; Indels 36; Gaps 4;
 Qy 1597 TACGGCTACATGGGTGGAGCGCGCTAGCTGATTCAGAGAGATGGCGCAAGGCTGTC 1656
 Db |||||
 Qy 4320 TACGGTCTACTAGGGCTATATCCAGAGGCGCGCTGCTACTCTACAGAGATGTCGAGAGCGGTA 4379
 Qy 1457 ACGGCTGGGGTAGGCACCTCATACGACGCATCATAC---ATAGCTGTGTAACTAGCG 1713

Db |||||
 Qy 4380 ACGGCTCTGGGAGAGGAGTATCATATCATGATGATCATATGAGGATATGAGGAAAGTACGCG 4439
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 Qy 1714 CTTATCGAATATGCTATGAGAAAGGTGTATCAAAAGCTTATCTTTACAGAGCGTAAGAG 1866
 Qy |||||
 Qy 4440 TTTAAGGTATCTATCAAGCAGACGCGATTTTTCGCACTACTCGAGCGATCT 4499
 Qy |||||
 Qy 1774 GAAATTTTCATTAATATTAAGAGAGGCTG--- 1806
 Qy |||||
 Qy 4500 GAAACCTGTAAGAGAGGCTATGAGTCTCTCATATATATATCAAGCGCAACTTCGCGC 4559
 Qy |||||
 Qy 1807 GGGTTCGAATATGCTATGAGAAAGGTGTATCAAAAGCTTATCTTTACAGAGCGTAAGAG 1866
 Qy |||||
 Qy 4550 GGGCTTTAGCTATGCTATGAGAGGCTTCTCAAAAGCGGCTTCT---CTGCGAGAGAG 4616
 Qy |||||
 Qy 1867 AGGTACGCTGGCTCTCTCGAGAGCGAGGTATAGATATGTCGTTTCTCGAGGCTGAGT 1926
 Qy |||||
 Qy 4617 AAGTATGCTGTATGAGAGAGAGGAGGAGGATATCAACAGCCGCGATCTGAGATGTGAGG 4676
 Qy |||||
 Qy 1927 GCGGATGCTGTGAGTCTCCCAAGAGGCTTCAAGTAAAGTGTGCAATATGATGAG 1986
 Qy |||||
 Db 4677 CTGCTGAGGAGGATATCAAGAGAGGAGGAGGAGGAGGCTTCTGAGCTTTGCTTAAAG 4736
 Qy |||||
 Qy 1987 ACGATGAGGTGAACAGGCTGTGAGAGTCTGAGAGTCTGAGAGATGTGAGAGGTGTGAGG 2046
 Qy |||||
 Db 4737 GACGCTGAGGCTGAGAGGCTGTGAGATGTGAGAGTCTGAGAGGATGTGAGAGGATGAGG 4796
 Qy |||||
 Qy 2047 GCGAGGCTCCATGAGAGGCTGTGATCTCGAGAGGCTTGTATCTCGAGAGGCTTGTAGG 2106
 Qy |||||
 Db 4797 TACGAGGCTCCGCGAGAGGCTGTGATCTCGAGAGGCTTGTATCTCGAGAGGCTTGTAGG 4856
 Qy |||||
 Qy 2107 TACGAGAGGAGGCTTGTGATCTCGAGAGGAGGAGGCTTGTAGGAGGCTTGTAGGAG 2166
 Qy |||||
 Db 4857 TACAGGAGAGGCTTGTGATCTCGAGAGGAGGAGGCTTGTAGGAGGCTTGTAGGAG 4916
 Qy |||||
 Qy 2167 GTTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2226
 Qy |||||
 Db 4917 ATACGCTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4976
 Qy |||||
 Qy 2227 AAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2283
 Qy |||||
 Db 4977 AAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5036
 Qy |||||
 Qy 2284 GTTACACCAATATCCCGCTGATATGATGATCTGGGTACTTGTGCATCCAG 2343
 Qy |||||
 Db 5037 ATTGAGACAGAGCTCTCCAGCCCTTGAGAGAGATCTGAGAGGCTCTGTTACCGGAG 5096
 Qy |||||
 Qy 2344 AGAAGACT 2352
 Db |||||
 Qy 5097 GAGAGCTG 5105

Search completed: November 26, 2003, 13:50:37
 Job time : 148 secs

db	178	DEIVNANVNSNPNRDPV11IGWTKCOK-QT-LANDYDGLAIGLRFVNFVQVDD11V	236
Qy	246	GNNHNRFDWPLLEPARIIGLIGLIVTRVQABPTTSVGHVSQGLNVDLYVYAEHPE	305
db	257	GVYVNFDPWPLLEPARIIGLIGLIVTRVQABPTTSVGHVSQGLNVDLYVYAEHPE	296
Qy	306	IKIKSHREBASTVYGVKMSHSERV11NMHRIIPDWDQDQPPFLLQYAPDQVATYGLAKI	365
db	327	VAVHEDNEDVYGVKMSHSERV11NMHRIIPDWDQDQPPFLLQYAPDQVATYGLAKI	356
Qy	366	LEPFAICISATVGLPDDQVGVHLEWILVIAKAPOKELVPESTVQVAVILE	425
db	387	IPFIEUITSIGPDDQVGVHLEWILVIAKAPOKELVPESTVQVAVILE	416
Qy	426	PLURCHVENANVLOSFSNPNV11KXNVPDLYVYVGHVGCSC-GCHPAVGVHFRPCP	484
db	447	PUPHIEHVYVLOSFSNPNV11KXNVPDLYVYVGHVGCSC-GCHPAVGVHFRPCP	470
Qy	485	GFBNVYVLELLELLELLELLELLELLELLELLELLELLELLELLELLELLELLEL	544
db	506	GLYVNNVLELLELLELLELLELLELLELLELLELLELLELLELLELLELLEL	529
Qy	545	CHECAVNAVHMLHIFRANVIAKGLVYVGHVTSVYVTDQVKNVFLIKELHGF	604
db	566	SKCEKAVNAVHMLHIFRANVIAKGLVYVGHVTSVYVTDQVKNVFLIKELHGF	588
Qy	605	EKLKSVYVLELLELLELLELLELLELLELLELLELLELLELLELLELLELLEL	664
db	626	ERKENVYVLELLELLELLELLELLELLELLELLELLELLELLELLELLELLEL	648
Qy	665	EVYNAVYVNAVYVKELEGVYVPEKIVNKTLSLEKSTLEPBAVHVAKMSLGVYTS	724
db	686	KYDVAIKYVYVYVFOLEVNFVLELLELLELLELLELLELLELLELLELLELLEL	708
Qy	725	PODKGVYVYVGVGHVGSORAPVYVYVYVQSGIDVYVYVYVYVYVYVYVYVYVYV	784
db	746	GVKVIYV	768
Qy	785	VASAKVQVLELLELLELLELLELLELLELLELLELLELLELLELLELLELLEL	800
db	806	769 K--TGQVYVLSFFX 781	

[illegible][illegible]

RESULT 5
 S75407
 Plasmid DNA-directed DNA polymerase (EC 2.7.7) - *Sulfolobus solfataricus*
 CDate: 11-Oct-1997 #sequence revision 44
 CSpecies: *Sulfolobus solfataricus*
 CUpdate: 11-Oct-1997 #sequence revision 44
 CAccession: S75407
 CAuthor: Singh, H. P.; Singh, R. K.; Allard, G.; Chan, C. Y.; Liu, Q. Y.;
 Mol. Microbiol. 22, 175-191, 1998
 Article: Organizational characteristics and information content of an archaeal
 AReference number: S73076; MUID:970555432; PMID:8899719
 AAccession: S75407
 ATitle: Plasmid DNA-directed DNA polymerase
 A Molecule type: DNA
 A Molecule sequence not shown; translation not shown
 AResidues: 1-764 >GENE
 ACross-references: EMBL:Y08257; NT:G707772; FID:g707813
 AExperimental source: strain 92
 AComment: This gene was submitted to the EMBL Data Library, Sequence
 CSuperfamily: herpesvirus DNA-directed DNA polymerase
 CSuperfamily: nucleotidyltransferase

[illegible]

RESULT 7

C75023
 DNA polymerase I PAB128 - *Pyrococcus abyssi* (strain Orsay)
 C:Date: 20-Jun-1999 #sequence_revision 20-Aug-1999 #test_change 20-Jun-2000
 C:Accession: C75023
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Reference number: A75001
 A:Accession: C75023
 A:Status: preliminary
 A:Residues: 1-771 <NM>
 A:Cross-references: GB:A748286; GB:A06836; NID:G545960; PID:G545913
 A:Experimental source: strain Orsay
 A:Gene(s): C75023
 A:Gene(s): C75023
 C:Superfamily: herpesvirus DNA-directed DNA polymerase

Query Match 28.6%; Score 1207.5; DB 2; Length 771;
 A:Residues: 1-775 <SD>
 A:Cross-references: GB:U07168; NID:G1197451; PID:AAA8769.1; PID:G1197452
 A:Status: preliminary
 A:Residues: 1-775 <SD>
 A:Cross-references: GB:U07168; NID:G1197451; PID:AAA8769.1; PID:G1197452
 C:Superfamily: herpesvirus DNA-directed DNA polymerase
 C:Keywords: DNA binding; nucleotidyltransferase

Query Match 28.6%; Score 1197.5; DB 2; Length 775;
 Best Local Similarity 36.1%; Pres. No. 5, 76-65;
 Matches 292; Conservative 150; Mismatches 285; Indels 91; Gaps 21;

Db 8 VLDSSEVQKGVQVINGANGRNVLRDSEFPFTALLAPADQPV---AQRIR 63
 2 ILTDYITENKKEIVAFVK-KENGEKFEYDAETFTFTALLKODSALDVKVKTAKSHG 60
 Qy 64 ALSRPSPIGVGEDDKKFKPRFRVRIKTVLPKAVREYVELVNDQVLEADRF 123
 61 KVR-----ITVENQKGLQRYEWMALZHPDPAIKETKRNPAVLFEDIFF 116
 Qy 124 AMRYLIDHLPFTMTVAEAPLENNGGFRVOKVILVSRPELYGALAPTKPLRL 183
 117 ARYVLDUGL-----TPWEN-----EELTFL 138
 Db 184 ARYLVYKQSPREDDPIVAIKTDGDEVI-----FIAEGDKDKPIREVEY 235
 139 AVDLTLEHSE--EFGQGIPTMISVADGKATVWSIDLPFVVSSEKEMIKLVY 197
 Qy 236 VKEVDPIVLGVGNHNPVLPARILAGILDTVTEVGAETPTVGH---VSVPG 292
 198 IRKVDPIVITNGNDPFPFLGAKALAPLAD--NSEPGMQDLSALVETKRI 256
 Qy 293 UNQVDVAEMPEIKLSLAEVLYGWKSKSEVINLWMEIDYWDQKPKPILQAY 312
 257 HFDLPVIRTNLPITPTLVANVAF--FGSKSEVYAH--EIAQMGSGEGLEVARY 311
 Db 335 DPAVYLAETLAKLPALQIKVYLPDQGVNGVGRLEWLPDPAQVMELVNVR 412
 314 EDATVTELGKEPMAGALQVQVVDVSGESVGVNVEFLKAYKNELEAKPEP 373
 Qy 413 RPE-----ETVGGATVLPDQGVNNGVSWHMKVYNGDPTVPEKGE 466
 374 EREYERLEKSEYEGYVKEPKLMGCVLSFSLPSIITHTVSPITANK--ENCKE 431
 Db 467 CQGMELPYNHFRFCRPFQKTVLERLLEKVAENAKYPPSPVLLDERQALK 526
 432 YDV--APQVGHCFKDFPGFPELLGLLEERQKEMEK--SKQVPEKLDVYRAIK 488
 Qy 527 VLAASVYNGVSGARCRCAQATAMGRHLRTAINARKGLKYGTUYSLFTV 586
 489 ILANSYVYVYAKANVCSGSSVINGNQYTDVRELESQRTNIDVLDVAT 548
 Qy 587 D-----PEKVENTIKIKEELG--FEIKLKYETKLEFTEAKRYAGLDEGRIDVG 637
 549 PQMKHEIKELQAVETNGVLPOLLLETETGPAQGV--TKCKVLTDEGRKVTNG 607
 Qy 638 FPAVGDQCLAKEVQTKVVIYKATSVBNKAVYKRVILEEGKVPTEKLVNKLTS 697
 608 LTIYVDSMEIKETAPVLAALAHGNDGVAIKVYEVTEKLSKYLIPPKLVITEG 667
 Qy 698 KRLSEYTTAEHVAAENMLSAGTVRSQDKGTVILVGGQKISQRAVPPYWK--DPS- 754

Db 668 RFSEYKALGHVAVAKLAAGKVKVKGWIGTVLEKDGPIEKRA---IAISEDPFK 724
 Qy 755 -QIDVTYVQMDQIPDAALPIYGYTETKKLSASATQ 791
 Db 725 KYDAEYTIENVQFAVERLQAGVYKDEALYQNTQ 762

RESULT 8
 S87920
 DNA-directed DNA polymerase (EC 2.7.7.7) - *Thermococcus* sp.
 C:Species: *Thermococcus* sp.
 C:Date: 7-Sep-1998 #sequence_revision 13-Mar-1999 #test_change 18-Jun-1999
 R:Southworth, M.S.; Kong, H.; Kucera, R.B.; Ware, J.; Janasch, H.W.; Perlter, F.B.
 submitted to the EMBL Data Library, January 1996
 A:Description: Cloning, expression and modulation of the 3'-5' exonuclease activity of
 A:Accession: S87920
 A:Gene(s): C75023
 A:Molecule type: DNA
 A:Residues: 1-775 <SD>
 A:Cross-references: GB:U07168; NID:G1197451; PID:AAA8769.1; PID:G1197452
 A:Status: preliminary
 A:Residues: 1-775 <SD>
 A:Cross-references: GB:U07168; NID:G1197451; PID:AAA8769.1; PID:G1197452
 C:Superfamily: herpesvirus DNA-directed DNA polymerase
 C:Keywords: DNA binding; nucleotidyltransferase

Query Match 28.6%; Score 1197.5; DB 2; Length 775;
 Best Local Similarity 36.1%; Pres. No. 5, 76-65;
 Matches 301; Conservative 139; Mismatches 256; Indels 97; Gaps 24;

Db 8 VLDSSEVQKGVQVINGANGRNVLRDSEFPFTALLAPADQPV---AQRIR 63
 2 ILTDYITENKKEIVAFVK-KENGEKFEYDAETFTFTALLKODSALDVKVKTAKSHG 60
 Qy 64 ALRFPSPFQVDDKDKFKTGRFPRVRIKTVLPKAVREYVELVNDQVLEADRF 123
 61 TVVKKR-----AEVYKGFLEPFWGLVFNHQPQVLEDAHNAVQVTEYDFP 116
 Qy 124 AMRYLIDHLPFTMTVAEAPLENNGGFRVOKVILVSRPELYGALAPTKPLRL 183
 117 ARYVLDUGL-----PWSG-----EELTFL 138
 Db 184 ADPIVSEVQKSPREDDPIVAIKTDGDEVI-----FIAEGDKDKPIREVEY 233
 139 AVDLTLEHSE--EFGQGIPTMISVADGKATVWSIDLPFVVSSEKEMIKLVY 195
 Qy 234 EYKVDPIVLGVGNHNPVLPARILAGILDTVTEVGAETPTVGH---VSVPG 290
 196 IRKVDPIVITNGNDPFPFLGAKALAPLAD--NSEPGMQDLSALVETKRI 254
 Qy 293 UNQVDVAEMPEIKLSLAEVLYGWKSKSEVINLWMEIDYWDQKPKPILQAY 312
 257 HFDLPVIRTNLPITPTLVANVAF--FGSKSEVYAH--EIAQMGSGEGLEVARY 311
 Db 335 DPAVYLAETLAKLPALQIKVYLPDQGVNGVGRLEWLPDPAQVMELVNVR 412
 314 EDATVTELGKEPMAGALQVQVVDVSGESVGVNVEFLKAYKNELEAKPEP 373
 Qy 413 RPE-----ETVGGATVLPDQGVNNGVSWHMKVYNGDPTVPEKGE 466
 374 EREYERLEKSEYEGYVKEPKLMGCVLSFSLPSIITHTVSPITANK--ENCKE 431
 Db 467 CQGMELPYNHFRFCRPFQKTVLERLLEKVAENAKYPPSPVLLDERQALK 526
 432 YDV--APQVGHCFKDFPGFPELLGLLEERQKEMEK--SKQVPEKLDVYRAIK 488
 Qy 527 VLAASVYNGVSGARCRCAQATAMGRHLRTAINARKGLKYGTUYSLFTV 586
 489 ILANSYVYVYAKANVCSGSSVINGNQYTDVRELESQRTNIDVLDVAT 548
 Qy 587 D-----PEKVENTIKIKEELG--FEIKLKYETKLEFTEAKRYAGLDEGRIDVG 637
 549 PQMKHEIKELQAVETNGVLPOLLLETETGPAQGV--TKCKVLTDEGRKVTNG 607
 Qy 638 FPAVGDQCLAKEVQTKVVIYKATSVBNKAVYKRVILEEGKVPTEKLVNKLTS 697
 608 LTIYVDSMEIKETAPVLAALAHGNDGVAIKVYEVTEKLSKYLIPPKLVITEG 667
 Qy 698 KRLSEYTTAEHVAAENMLSAGTVRSQDKGTVILVGGQKISQRAVPPYWK--DPS- 754

Db 1 MEDRYMLDIDVYTVDEVPVIRLFOKOKSGNEPIIANDRSFVIAL-----PTDL 54
 Qy 59 AQRITAKSPKSTIOEDKKYKFORRRVLITVTPAAYREYELVWGVQDVLE 118
 Db 55 DECLAELELEKLELVN--NRGLRPTVEITFEHQVQVTKIDHLESDVDE 112
 Qy 119 ADRPAMRVLIDHLPF-----FTWVRNRPLEHOGGRVQKVLVGNRPPLGELA 173
 Db 113 HOLIPETRLIDVIMBEELFQGVGDSAPVTVTVETVGVQSTGSGM--- 168
 Qy 174 PTKLDELRLADIEVSKSGPSPDPVIVATK-----TDGDPVLPTAGSD 224
 Db 169 -----LQLSPIDLVNRPNGPDEIDELVHLCGACNGVSVSTAGHDLPTVEVD 222
 Qy 225 DRKPEFVEVETKATDPTLVGNHHPDMPYLLERARLIGLQV-----TERVGA 276
 Db 223 EELLESFAVLIDVIGNSDPPFIITNADNLOEALDGGOSTKTERGF 282
 Qy 277 PPTFVHGVNVRGLVLDVYAEEMPEIKISLEEVAVLGWNGKSERVINMHPD 336
 Db 283 ANNTAKNGV-----HVLDPYWRKMLORTLERYQLFQSEKIDLPORLME--- 333
 Qy 337 YHDDPKRGLLQVARDQNTVGLAEKLPALGPAIGLVGVLGDQVMSVGPLRML 396
 Db 334 YHOREDLRGLFVLDVYVHAKELRLPLMLRLVGLVDFQFDSIMATQQQEWEL 393
 Qy 397 TAAVQKGLVPLNVRPDEETV-----GALVPLGAGHENTVLDPSGMYNTIKY 450
 Db 394 VKACVQGLVPLNPGQSGSSRRGAVGVYKPEGLHENTVQDFSLVPIITISK 453
 Qy 451 NVGPTTIVPGKQGCQWAEVHVRFCPPFTVLELLELVAVRBAVKYPP 510
 Db 454 NISPTTIDDEES-----ECYVAPVGYTRFKSPFVSVIGETLSENVKIEEMG-SD 508
 Qy 511 DSEVPLIDRQKALVANSYNGWNGKSGVQSGVQGVNAYTANGHRLIPTALIMKL 570
 Db 509 DEWEKILANVQGLALVNTVGVYGFRTFVSMELCAELITWAGDVIKTKITAEF 568
 Qy 571 GLAVYVQTPGSLFTV 586
 Db 569 GSHTVADTDFATY 584

Query Match

Best Local Similarity 18.3%

Matches 246; Conservative 160; Mismatches 319; Indels 177; Gaps 30;

Qy 3 RVVFTVLSVSVGKPEVQVITNGATGKGVLLDRSEFFVFLALPAGDPKVAQRI 62

Db 97 DTVFQGLDEFTTSVSLRFLQVNGNSLVNNGVQFPTFYVAPVPRFELMT 156

Qy 63 NAL-----SRPKSVFGDEKKYKGRPRVRLITPLE 98

Db 157 QDADATCGVGHDIKCIEMKNLVQFGCKESEPFIK-----FTTNKILSRANVPER 210
 Qy 99 AVRYEYELVWGVQDVLEADRANRVLRLIDHLPFTVYEAFLNPGGVN--- 154
 Db 211 GENFSELFPGVGV--TTSESTVQVLFMDLQWGVNHLPSKQVQHYGVNCSQ 269
 Qy 155 -----DAVTLNRSRPFYVLSGALAPTKLPDRILAPVIVSKQ--SPREDDPV 205
 Db 270 IEMINVDLISL-----PAEQW--SKAPALALISFIDISCGRPFDPDSIDPVIQ 320
 Qy 306 ILA-VTQDQGVFLFA-----SEGDORRPFREFVYVYKVPDPIIVGY 247
 Db 242 IASVYQGSTGTFPANNVCTVQSCVQVGVTFQWGLMSNSKFPVQDVLVLIG 380
 Qy 380 NNHHPDMPYLLERARLIG--KLDVTRVGLAEPFTSVGH-----VSVFQRLN 293
 Db 381 NTCNDPFIIDLRQKALVANSYNGWNGKSGVQSGVQGVNAYTANGHRLIPTALIMKL 440
 Qy 294 VLDVYAEEMPEIKISLEV-AYELGWKCKSERVINMHPDYM--DPKRPPLQ 349
 Db 441 LMLQVARDQNTVGLAEKLPFA--TOLSVYTGVLGDQVMSVGPLRMLITAEAPKFLV 494
 Qy 350 YARDVQNTVGLAEKLPFA--TOLSVYTGVLGDQVMSVGPLRMLITAEAPKFLV 407
 Db 495 YCLMAYLPQRMDKCMFVETARVGVYVFFLLARQGVKVISQFPAQLQHDV 554
 Qy 408 PN-RVRSRPFETGAILVPLRQVHEN-IAVLDSSMYPTNK----- 447
 Db 555 FNTVNGVQGLATVETKPIFYDPTIATDLSLSYLSMQANLVCTYLLDSNIAEL 614
 Qy 448 -----IKYWDGP--DTLVYRGEKSGCEGWEAEVHVRFCPPFTVLELLEK 499
 Db 615 LKIKQDVTSYTFNGDGVFKPHVR-----KLLPILADLADLARK 654
 Qy 500 RVRAEKVTFPSEFVLLDRQKALVANSYNGWNGKSGVQSGVQGVNAYTANGHRL 559
 Db 655 KARADULK-ETDPFKAVLDGRQALKVANSYVGTGTATGSLPLAISSTVSGRM 713
 Qy 560 IPTAHNARK-----GLATVNGTSPSLFTTDSKENVFKIIEELGF-- 604
 Db 714 IETKDVVKEKRYENGQSHQVNIYDTSQWAKGVKTFEALMGSEANTVSDQPP 773
 Qy 605 ---SIKLVNKLGLPFTFAKNVALL-----EDGIDVGVRAVDQCLAKVQTKV 656
 Db 774 NTKLFSEKVFYF-YLISEKRVGLFWTDTTQNGSKGLTVRNDCTVSYVIDTA 832
 Qy 657 VRYLTVSEKNAVYVRYVLEKRGQPKVTKVNTLSKLEBETTFEAPHVALEM 716
 Db 833 LKMDLQDQGVQFVTSKDLQKNSQVLTALK--TDYAKAVNVLSELM 890
 Qy 717 --LEAGTVSPKGTGVTVG--GRISORAW-PYFMVQSDQSDVTVYVDHQTAL 771
 Db 891 RKSDGSSALQGRVAVIILQDQGVVASEPDPVIVENPITDKNTLNLQSKPL 950
 Qy 772 RI 773
 Db 951 NI 952

RESULT 13

DNA-directed DNA polymerase (EC 2.7.7.7) KOD, intein containing precursor - Pyrococcus

N; Contains: DNA endonuclease (EC 3.1.-.-) P1-1; DNA endonuclease (EC 3.1.-.-) P1-17; D

C; Species: Pyrococcus sp.

A; Variant: 72; strain KOD1

C; Accession: J01551

C; Accession: J01551

R; Kakiura, H.; Takagi, M.; Imanaka, T.

submitted to the EMBL Data Library, March 1994

A; Description: Cloning and analysis of the DNA polymerase gene from a new hyperthermophilic

A; Accession: J01551


```

Qy 306 IKIKSLERVA-EYLGWVKSERVIINWWEIPDYMDPKRPIILQYARDVR--ATTGL 361
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 469 LRSHTLNAVSPHJBJQXEDQHSI-----ITD-----LQNGDQTRRLAVTCL 513
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 362 AKILPF-----AIOLESYVTGLDQVAMSVGRLEWYLITRAAFKMKELVNR 410
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 514 KXALPULLLELWLVNAVEMARVOTPLSLHSRQQVKNVSQLKQNHGLLPVV 573
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 411 VERPEETRGAVLEPREGVHE-NIANLDFSSNPMIMIXYNGPDLVRPG--EKGCBC 467
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 574 KSGGSDTGVAVIEPPLGTYDVPJALHDFSSLVFSLIMAHNLCYTLRLRGTACKLG-- 631
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 468 GCMWAEPEVHERPCFPG--FEFT-----VLERLELRKRYAEMKYPDPSEYR 516
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 632 -----LTDQIIRFTTSDPEFVTSVAKGLLPQILENLSAKRKAABLAK-ETDPLERQ 684
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 517 LLDBROKALVANSYGMWGSGRWYCRCAKAVTANGRELI-----RTAINIA 567
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 685 VLDGRQLANVANSVYGTGAQVGLKPLCLEISQSVTGFGRQMIKTKQLVSKYTVENG 744
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 568 RKLZLVXVYGDTSPLVTVDPDENFTKIKKELOF-----EYKLRKYKELFT 618
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 745 YSTSAKVYVYDTSVMCRFGVSSVAEMALGREAADWYSGHPSPIRLSPFKYYP-YLL 803
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 619 EAKRYVAGLI-----ECCGTDYQCEKAVNGKCELAKVOTKRVELVKTSEVNAVEY 672
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 804 ISKRYAGLIFSRPDADHDMDCGLNVRDNCFLVANLVLTASLRLLIDREKAVAH 863
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 673 VRKYVKELEGAPTEKLVYKNTLKRLEBETTEREHRVAVNM--LSAGVYVSPDKIG 730
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 864 AOVISLLEONIDISQVITKELTRASDYAGQAHVELAEMERKDPSSASLGRVP 923
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 731 YVIV--KCGGRISQAMFYWKDPSPQIDWTVYVHQHITPAARI 773
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 924 YVLSAAGVAVWKSDELFVLENSLPIDQYVLEQVAKELJLI 969

```

Search completed: November 25, 2003, 15:00:30
 300 lines : 21 5868

[illegible]

GN POL OR POLA.
OS Thermococcus gorgonarius.
OC Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OX NCBI TaxID=11997;
RN [1] -
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RA Thermococcus gorgonarius; 963600-3605(1999).
RA Huber R., Angerer B.; 1219-1223(1999).
RT "Crystal structure of a thermostable type B DNA polymerase from
RT Thermococcus gorgonarius".
CC CC-1. FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE
CC EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC CC-1. CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC CC-1. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
CC PDB; 1TGO; 22-MAR-99.
DR InterPro: IPRO06117; DNA_pol_B.
DR InterPro: IPRO06134; DNA_pol_B_dom.
DR InterPro: IPRO04570; Pol_B.
DR InterPro: IPRO04570; Pol_B_exo.
DR Pfam: PF00136; DNA_pol_B_1.
DR Pfam: PF01104; DNA_pol_B_exo_1.
DR SMART: SM00486; POLB; 1.
DR TIGRFAMs; TIGR00592; pol2; 1.
DR PROSITE; PS00115; DNA_POLYMERASE_B; 1.
DR KEGG; 3D-structure; DNA-directed DNA polymerase; DNA replication;
KW DNA; Nucleotides; Nucleic acid; Nucleoside; Nucleoside; Multifunctional enzyme;
FT DISULFID 428 442
FT DISULFID 506 509
FT STRAND 11 12
FT TURN 11 12
FT STRAND 13 22
FT TURN 23 24
FT STRAND 25 31
FT TURN 32 33
FT STRAND 34 47
FT HELIX 48 51
FT TURN 52 53
FT STRAND 54 59
FT TURN 60 61
FT STRAND 62 64
FT STRAND 67 75
FT STRAND 76 87
FT TURN 88 91
FT TURN 90 91
FT HELIX 92 102
FT TURN 104 105
FT STRAND 106 112
FT HELIX 116 123
FT TURN 124 125
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FT STRAND 165 166
FT TURN 167 172
FT STRAND 179 180
FT TURN 181 182
FT HELIX 187 201
FT STRAND 205 208
FT STRAND 211 213
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FT STRAND 248 251
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FT STRAND 255 259

FT HELIX 260 267
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FT TURN 308 317
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FT STRAND 448 469
FT HELIX 473 480
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FT TURN 503 504
FT HELIX 507 530
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FT HELIX 553 568
FT TURN 569 570
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FT STRAND 577 590
FT TURN 591 592
FT STRAND 593 597
FT STRAND 603 606
FT STRAND 615 615
FT STRAND 617 617
FT HELIX 617 631
FT TURN 632 651
FT HELIX 632 651
FT TURN 652 653
FT HELIX 657 659
FT STRAND 662 665
FT STRAND 670 670
FT HELIX 679 685
FT TURN 690 690
FT TURN 695 695
FT TURN 706 706
FT STRAND 716 716
FT STRAND 717 719
FT TURN 722 724
FT STRAND 729 735
FT TURN 736 737
FT HELIX 738 740
FT TURN 741 741
FT TURN 747 749
FT HELIX 752 754
FT TURN 766 767
FT TURN 773 773
SQ SEQUENCE 773 AA; 89812 MW; F67AF048575FB644 CRC64;

Query Match . 29.7%; Score 1245.5; DB 1; Length 773;
Best Local Similarity 36.1%; Pred. No. 9.9e-71;
Matches 300; Conservative 148; Mismatches 289; Indels 93; Gaps 21;

466 ECGCCE--APRVGHRFCPPGFKTVLELLEKRVADWAKYPPDSPEYRLRQ 522
 Db 427 --CGCTVAPGVRGCTGPPGFLGGLGGLGGLGGLGGLGGLGGLGGLGGL 483
 QY 523 KALKYLANASVYGVGSGARVYCRSCAMATAGRGHLRLA--NIARKLVNIVYDTS 581
 Db 428 KALKYLANASVYGVGSGARVYCRSCAMATAGRGHLRLA--NIARKLVNIVYDTS 581
 QY 584 RAKYLANASVYGVGSGARVYCRSCAMATAGRGHLRLA--NIARKLVNIVYDTS 581
 Db 429 RAKYLANASVYGVGSGARVYCRSCAMATAGRGHLRLA--NIARKLVNIVYDTS 581
 QY 582 LFVYVY--DSE--KVENFKIKKELQ--FKIKELVYKSLPFTFAKRVAGLDR 632
 Db 544 LHMATFQADAEVKKAKSEFKYINPKLKGLELETFSTVGGFV--TKKAVIDSEK 602
 QY 633 IDLGEFVAGVGCCLAKEVGVGVVYVVKVGVGVGVGVGVGVGVGVGVGVGVGV 692
 Db 603 IDLGEFVAGVGCCLAKEVGVGVGVVYVVKVGVGVGVGVGVGVGVGVGVGVGV 692
 QY 693 YWTKLGLSEFTTARVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 752
 Db 663 HQHQLTRDYVATGHVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 721
 QY 753 PS--QDVTYV 803
 Db 722 FTHRVDAEYV 774
 RESULT 9
 ID DPOL_METVO STANDARD; PRT: 824 AA.
 DC P52025-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA polymerase (EC 2.7.7.7).
 OS Methanococcus voltae.
 CC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 CC Methanococcaceae; Methanococcus.
 RN J01741;taxid=2186;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95014087; PubMed=7923013;
 RA Konisky J., Paule S.M., Carnato M.E., Kasey J.M.;
 RL "Bacterial polymerase gene from the methanogenic archaeon Methanococcus
 RL J. Bacteriol. 176:6402-6403 (1994).
 CC -1- [CHN]N. BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
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 CC or send an email to license@isb-sib.ch).
 DE ENBI; L33366; RAA72443.1; --
 DR HSP; P56689; ITCO.
 DR InterPro; IPR005172; DNA_pol_B.
 DR InterPro; IPR005131; DNA_pol_B_dom.
 DR InterPro; IPR004578; POL2.
 DR Pfam; PF00136; DNA_pol_B.
 DR Pfam; PF03104; DNA_pol_B_ext; 1.
 DR SMART; SM00486; POLB; 1.
 DR TIGRFAMs; TIGR00592; pol2; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 KW DNA polymerase, DNA-directed DNA polymerase; DNA replication;
 DE SEQUENCE 824 AA; 96754 MW; 09A630D8C151FC CRC64;

Query Match

Beat Local Similarity 23.5%; Score 986; DB 1; Length 824;
 Matches 255; Conservative 199; Mismatch 288; Indels 178; Gaps 25;

QY 9 LDSEYVVG--KEPQVLIKAENGVRVLDSEFTVYFALLARQDVQVQAQIRAS 67
 Db 12 IDMYTONGGLAKPEINQCE--FKPFYF--VDSPEKELYDGLQNG 57
 QY 68 -----PK-----SPTGVDRKQVYRFR 88
 Db 58 ETDKAKLEPEFENATSLKYQDLTNIETIKVSYDMLNGKSEVSPKAK--KSK 114
 QY 89 VLRIVLVPEVRELVNVDGVQVLEIAHFAHMY--IDHLPFPFVTRVSEFAS 148
 Db 115 ICKVYKTVNFKVILREYKESG--KSYFPIPLFPLRMIDQIVSAAKS--EDKIN 170
 QY 149 KMGFRVQVLVSRRPEPLVGEALPALTPLDRLAEDVSEKSGSPRPDRPVIAY 208
 Db 171 -----SPLFENLSEHEDKSTK--FNWAKQDFLWNL 202
 QY 209 KYDDQEVL-----FIABGQDKAFREFTVYVYDQDVIWNNHDFPY 256
 Db 203 FSKDYQVYKVFENSEVNGVDYKSEILQRTILQI--DYITTINGNDPFP 260
 QY 257 LPARAILGLDQVTRVQVAPPT--SVHGVSVFQRLVLDVYAEEMPRKIK 309
 Db 261 LAGANVITDEVDNAGSQQPQIKYSGQKINSEKIPQILHDPITAKRLMK 320
 QY 310 SLEAVELQWVGKSERVINNWEIPDYVDWPKPQLQVARDVATVGLAKLFLPA 369
 Db 321 KLENVYQLFAPK--ANDYQDIPQW--TEUTLFLAVDALTYKGNVYFLE 375
 QY 370 IQLSVYTGLPDDGVNSGVGLEWLYLFAAFKMLVNRV-----RPSTVGAIV 423
 Db 376 INFRVYVQPYDPSRNSQWSPFLKSKFQNIWSPSSSYREAFKSYEGTV 435
 QY 424 LPIQGVHENTVLDPSNYPNIMKYNGPDLVREKSGCGOQVREYVHFRCF 483
 Db 436 REPAGIQSDVLELQPMVSLFSLIGNISFPIYV-----SEK--EME 480
 QY 484 POFKTVLSLELEKREVRK--KYPDPSPVYLDSEKLYALVAGVWGWS 539
 Db 481 LQIIPITMELLSRGHKKMLQKQNEFQ--EYSELEHKSQVLANSHGLTAF 539
 QY 540 GAGQCBQCNVAGRGHILHAIHARGVILGVIVQDTSIVFYVYKRV 592
 Db 540 MARVSDKCAWYTGRLARKVQETKEAKSEFKVIATDGFYAKWYDKLGKXEN 599
 QY 593 -----NFKIKSEK--GFIKIKVNR--LPTFAKKYVAGL 627
 Db 600 DSDKSLSEPLSKSEILITKPLAGINELPEGLMELFHFPGFLAVT--KXVALI 657
 QY 628 LDDGVKFGKSGKELANVQVIVLMTSEVNAVYVAKIVQIEKRPV 687
 Db 658 EDQHVIVGVLEVRDINSAGVQVATALLSEQDVLNKLKINTQNLAKENIK 717
 QY 688 ELVYKTKLSKLSLETTEDPVAWAKMGVSGFQDKQVTVVKGQISQAPAY 747
 Db 718 NDLHQLQINLEIKYKSTALHVAWAKVQGVNVQVDSIIIVKSGRISER---- 774
 QY 748 FNVKQPSQIDVTIVYDRIIPALRITGFGITKELKKS 787
 Db 775 ELUATVADDVDIYDQVQVYVIRMSLSISELANS 814
 RESULT 10
 ID DPOL_PYSND STANDARD; PRT: 1312 AA.
 DC Q51334; Q51335; Q51336;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE DNA polymerase (EC 2.7.7.7) (Deep Vein DNA polymerase)
 OS DNA polymerase (EC 2.7.7.7) (Deep Vein DNA polymerase) [Contains:

QY 571 QKVIYGDISLVTV 586
 Db 569 GHVTVADISPTV 584

RESULT 13
 IDOL_THERM STANDARD: PKT; 1523 AA.

DR 15-DEC-1998 (Rel. 37, Created)
 DT 28-FEB-2003 (Rel. 47, Last sequence update)
 DE DNA polymerase (EC 2.7.7.7) (pol Tfu) [Contains: Endonuclease PI-TfuI
 DN (EC 3.1.-.-) (Tfu pol-1 intein); Endonuclease PI-TfuII (EC 3.1.-.-)
 GS (Tfu pol-2 intein)].

OS Thermococcus funiculans; Thermococci; Thermococcales; Thermococcaceae;
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 RN 1183_Taxid:46540;
 RN 1183_Taxid:46540;
 RC SEQUENCE FROM N.A.
 RC STRAIN-ST557;
 RC Cannon M., Querelle J.,
 RN Submitted (FEB-1996) to the EMBL/GenBank/DBS databases.
 RN CHARACTERIZATION OF INTEINS.

RC STRAIN-ST557;
 RL MEDLINE=2012788; PubMed=10644693;
 RT "Inteins of Thermococcus funiculans DNA polymerase are endonucleases
 with distinct enzymatic behaviors."
 RL J. Biol. Chem. 275:2335-2341(2000).
 CC base pairs. (b) TfuII recognizes and cleaves a minimal sequence of 16
 CC 19-bp minimal recognition sequence. The optimal temperature for
 CC FUNCTION= 87.7 degrees Celsius. active homing endonuclease using
 CC Mg(2+) as cofactor. Its minimal recognition and cleavage site is
 CC 21 bp long either on linear or circular DNA substrates. Its
 CC endonuclease activity is strongly inhibited by the 3' cleavage
 CC strand and the 5' cleavage site. The enzyme after the cleavage
 CC reaction. The optimal temperature for activity is 70 degrees
 CC Celsius.

-1. CATALYTIC ACTIVITY: N deoxynucleoside triphosphate + N diphosphate
 -1. PFM THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
 A POST-TRANSLATIONAL EXCISION OF THE TWO INTERVENING REGION
 (INTEINS) FOLLOWED BY PEPTIDE LIGATION.
 -1. SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
 -1. SIMILARITY: BELONGS TO THE INTEIN SECTION; BELONGS TO THE HOMING
 ENDONUCLEASE FAMILY.

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 or send an email to license@isb-sib.ch).

EMBL; Z69882; CA93738.1; .
 DR HSSP; P56689; 1TGU.
 DR RELEASE; 4500; PI-TFUI.
 DR 1183_Taxid:46540;
 DR InterPro: IPR006172; DNA_pol_B.
 DR InterPro: IPR006134; DNA_pol_B_dom.
 DR InterPro: IPR006133; DNA_pol_B_exo.
 DR InterPro: IPR001586; Hedgehog_HhncC.
 DR InterPro: IPR001587; Hedgehog_HhncC.
 DR InterPro: IPR006141; Intein.

DR InterPro: IPR006142; Intein.
 DR InterPro: IPR004042; Intein_endomuc.
 DR InterPro: IPR004578; pol_2.
 DR Pfam: PF00156; DNA_pol_B_2.
 DR PRINTS: PRO0379; Intein_260.1.
 DR SMART; SM00305; HhncC; 2.
 DR SMART; SM00306; HhncC; 2.
 DR TIGRFAMs; TIGR01443; intein_N_term; 2.
 DR TIGRFAMs; TIGR01445; intein_C_term; 2.
 DR TIGRFAMs; TIGR00592; pol_2_1.
 DR PROSITE; PS00119; INTEIN_260_1.
 DR PROSITE; PS00119; INTEIN_260_2.
 DR PROSITE; PS00119; INTEIN_260_3.
 DR PROSITE; PS00119; INTEIN_260_4.
 DR PROSITE; PS00119; INTEIN_260_5.
 DR PROSITE; PS00119; INTEIN_260_6.
 DR PROSITE; PS00119; INTEIN_260_7.
 DR PROSITE; PS00119; INTEIN_260_8.
 DR PROSITE; PS00119; INTEIN_260_9.
 DR PROSITE; PS00119; INTEIN_260_10.
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 DR PROSITE; PS00119; INTEIN_260_95.
 DR PROSITE; PS00119; INTEIN_260_96.
 DR PROSITE; PS00119; INTEIN_260_97.
 DR PROSITE; PS00119; INTEIN_260_98.
 DR PROSITE; PS00119; INTEIN_260_99.
 DR PROSITE; PS00119; INTEIN_260_100.

[1] SEQUENCE FROM N.A.
 RP MEDLINE:92071954; PubMed:196073;
 RA "Characterization of the POU3A and POU3F1 genes and their expression patterns in embryonic stem cells." [2]
 RT pombe indicates inter-species conservation of the catalytic subunit
 RT of DNA polymerase delta." [3]
 RW Med. Biol. 222:209-218(1991).
 RP SEQUENCE FROM N.A.
 RP MEDLINE:93184400; PubMed:843413;
 RA Park H., Francesconi S., Wang T.S.F.;
 RT delta from Schizosaccharomyces pombe." [3]
 RL Mol. Biol. Cell 4:145-157(1993).
 RP SEQUENCE FROM N.A.
 RP MEDLINE:97184901; PubMed:1185930;
 RA Wood V., Williams R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
 RA Spours J., Peat N., Hayes J., Baker S., Baham D., Bowman S.,
 RA Collins M., Connor R., Cronin A., Davison P., Fairclough D., Churcher C.K., A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K.,
 RA James S., Jones L., Jones M., Leathers S., McDonald S., McLean J.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Stevens K.,
 RA Woodward J., Volkert G., Wertz R., Wertz S., Wertz T., Wertz U.,
 RA Wajsbom I., Vansteelandt G., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Mosel D., Hilbert H.,
 RA Broyer J., Zanger I., Beck A., Leinhardt R., Pohl T.M.,
 RA Goffeau A., Cadieu E., Dreesen S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert P., Aves S.J., Xiang Z., Hunt C., Moore K., Ruet S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garson A., Rhode G.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Porchias G.,
 RA Curretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovskiy G.V., Ussery D., Barrell B.G., Nurse P.;
 RA Nature 415:871-880(2002).
 [4] SEQUENCE OF 272-455 FROM N.A.
 RP MEDLINE:92022466; PubMed:1075989;
 RA Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
 RA Hirose Y.;
 RT large-scale screening of intracellular protein localization in living
 EL cells using a GFP-fusion genomic DNA library." [4]
 CC -1- FUNCTION: THIS POLYMERASE POSSESSES TWO ENZYMATIC ACTIVITIES:
 CC DNA SYNTHESIS (POLYMERASE) AND AN EXONUCLEOTIC ACTIVITY THAT
 CC CRYSTALLIZES SELL STAMPED DNA IN THE 3' TO 5' DIRECTION.
 CC -1- CRYSTALLINIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + [DNA] (n)
 CC -1- SUBUNIT: HETEROTETRAMER THAT CONSIST OF THE POL3, CDC1, CDC27 AND
 CC CMH SUBUNIT. THE POL3 SUBUNIT CONTAINS THE POLYMERASE ACTIVE
 CC SITE. CMH MOST LIKELY THE ACTIVE SITE FOR THE 3'-5' EXONUCLEASE
 CC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
 CC POLYMERASE ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR
 CC DIFFERENT TYPES OF DNA REPLICATION.
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
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 CC -----
 DR ENBL; X52525; CAA35308.1;
 DR ENBL; L07734; AAA35308.1;
 DR ENBL; AL421815; CAB81556.1;
 DR ENBL; AB027796; BAA87100.1;
 DR PIR; T40342; T40342.
 DR PIR; T40342; T40342.
 DR PIR; T43266; T43266.
 DR GeneDB_Spombe; SPBC336.04;
 DR InterPro; IPR006172; DNA_pol_B.
 DR InterPro; IPR006172; DNA_pol_B.
 DR InterPro; IPR006133; DNA_pol_B.
 DR InterPro; IPR004578; Pol2.
 DR InterPro; IPR004578; Pol2.
 DR Pfam; PF00136; DNA_pol_B.1.
 DR SMART; PF0104; DNA_pol_B.
 DR SMART; PF0104; DNA_pol_B.
 DR TIGRFAMs; TIGR005921; pol2.1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B.1.
 RM Transferrase; DNA-directed DNA polymerase: DNA replication.
 RM Transferrase; DNA-directed DNA polymerase: ZINC finger; Nuclear protein.
 FT TRANSFERRASE; 193; 101;
 FT ZN_FING; 1040 1058
 FT C4_TYPE (POTENTIAL).
 FT Q -> E (IN REF. 1).
 FT Q -> E (IN REF. 4).
 FT CONFLICT 102 102
 FT CONFLICT 290 290
 FT CONFLICT 419 419
 FT CONFLICT 545 545
 FT CONFLICT 777 784
 FT KLEFVKY -> NKSFST (IN REF. 1).
 FT CONFLICT 866 866
 FT L -> H (IN REF. 1).
 FT CONFLICT 1068 AA; 12568 NM; 9952841320C3CA CRC64;
 SEQ SEQUENCE 18.44; Score 771.5; DB 1; Length 1086;
 Query Match
 Best Local Similarity 27.3%; Pred. No. 9e-41;
 Matches 246; Conservative 160; Mismatches 319; Indels 177; Gaps 30;
 QY 3 EVPTVLDSYEVVCKEDPVTWNGIANGERVLLDSFPTVALLAGADPQVADRT 62
 DQ 97 IYVQIDISEFTSEVSFIRLVGVNVDNGNSLVHVGVLFFVPAVQVGFPELSEFT 156
 DQ 63 RAL-----PABEQN-----SQAELAFMSDFACAGKGVDFPDSIDVIO 320
 DQ 93 DYI-----PABEQN-----SQAELAFMSDFACAGKGVDFPDSIDVIO 380
 DB 157 QDLATGNGGVGDICIKEMENYGFQGNKSPFTK-----FTNPTLSLRNVFV 218
 QY 99 AVREYELVNVGVDEVLADIPAFYVILINDLPFPTVTVVELEKNGKGV----- 154
 DB 211 GFNPFELFPGVGV--TFTESTVYLLAFVDFCDVGVGVHLPASKVQVQVNRVSNQ 269
 QY 135 -----DKVTLVSHFSEVKNALATPGLDPLADPTEYVSKQ--GPPRQPVTV 205
 DB 270 IEAMVTKDLSL-----PABEQN-----SQAELAFMSDFACAGKGVDFPDSIDVIO 320
 DQ 206 TA--WDGDDGVETLA-----EGDGRKPIRENVKRVDPDVLIVV 247
 DB 321 IASIVTVQGVSTFVFNVCVQSVGVGVTFQNGAEMLSNKKVDFVDVLIVV 380
 QY 248 NNNHNVNVLARALHIG-----KDVYRFGVAGETTVGVH-----VSVFGML 293
 DB 381 NNHNPFDPLDNRANSLEHNFELGRHNFVSKETTSNVGVRESKTVL--PQLQ 440
 QY 294 VLDVYAEHMPKIKLSLEY--ASYLVGMNSRVINNHEDVMD--DPEKGLIQQ 349
 DB 441 LNNVQVQDFKELSVLNVCSQFQDQED-----VHSIITLQVADNR--LAI 494
 QY 350 YARDVATVYGLAKELPFA--IQALVYVPLDQVGMNSVGLFVLTAAFKMEKLY 407
 DB 495 YLCAVLPQPMKDLKCFVNTTBMATVQVNFELLAGQKVIISQIFRAQGVHIVV 554
 QY 408 PN--RVEPEETVGAIVLFLGVGHN--IAVDFPQNSVYRIN-----VST 447
 DB 555 PAIRVNGTGVGTATVETPIGVYGVTVITLDFPSSLYVHQAHHNVCTYLLDSVTAEL 614

Search completed: November 25, 2003, 14:59:02
Job time : 27 sec8

542 RYTCRCAMVANGRLHRTAINTAKIKLVKIVGDTLSLTVYDPEKVENPIKKE 601
 546 RYTCRCAMVANGRLHRTAINTAKIKLVKIVGDTLSLTVYDPEKVENPIKKE 584
 602 LGFEIKELKIVYFEAKKRIYAGLEGRIDVGFSAVRCMDKALAEVQVKEIVL 661
 585 YGLIDKIDKATYVFEAKKRIYAGLEGRIDVGFSAVRCMDKALAEVQVKEIVL 644
 662 KTSBWKV-----VEVVKVLEKGVKIVKIKVLSKLEVEYFEAPVAAKWL 717
 645 KQDITVARGVYKIVKIKVYKIVKIVKIVKIVKIVKIVKIVKIVKIVKIV 704
 718 SAGTVSGDKVIGVVKGGRIKIVKIVKIVKIVKIVKIVKIVKIVKIVKIV 777
 705 RGRVYVGGTIGVVKGGRIKIVKIVKIVKIVKIVKIVKIVKIVKIVKIV 704
 718 GTEKELKASVGG-----OKTLEFDTA 799
 765 GYKESDLK-----TGMERSLIDPLS 765
 RESULT 6
 Q959K4 PRELIMINARY; PRT; 775 AA.
 AC Q959K4_2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE DNA polymerase (EC 2.7.7.7).
 OS Archaea: Euryarchaeota.
 OC Archaea: Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 SK NCBI_Taxid:74610;
 RP SEQUENCE FROM N.A.
 RC STRAIN=AL585;
 RA Querrelon J., Cambon M.A., Lesongeur F., Forterre P., Barbier G.;
 RT Thermococcales and phylogenetic implications "belonging to
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC -/- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N DIPHOSPHATE
 CC -/- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
 DR EMBL; AJ004834; CAB81809.1; ..
 DR HSP; P56689; ITGO.
 DR InterPro; IPRO06172; DNA_pol_B
 DR InterPro; IPRO06173; DNA_pol_B_dom
 DR InterPro; IPRO06133; DNA_pol_B_exo.
 DR InterPro; IPRO04578; Pol2_..._exo.
 DR Pfam; PF00136; DNA_pol_B_1.
 DR PRINTS; PR01060; DNAPOB-exo; 1.
 DR SMART; SM00486; POLB; 1.
 DR TIGSFams; ITIG00592; pol2; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 DR PROSITE; PS00117; DNA_POLYMERASE_B_1.
 KW Nucleotidyltransferase; Transferase;
 SE SEQUENCE 775 AA; 90492 MW; 677264920D770C0F CRC64;

Query Match 30.3%; Score 1248; DB 1; Length 775;
 Best Local Similarity 30.5%; Score 1248; DB 1; Length 775;
 Matches 304; Conservative 154; Mismatches 278; Indels 98; Gaps 23;
 8 VLDSGSGSPFVINGIANGRGVRLVINDSPRTFALLAGAPQVY----AQR 63
 2 ILDDVITGSGPRTIFPKRGVRYVDFVDFVDFVDFVDFVDFVDFVDFVDF 60
 64 ALSRPSKSTIGVEDDKRGVRYVDFVDFVDFVDFVDFVDFVDFVDFVDF 123
 61 KIVR----LUDVKNVKGKGLFVDFVDFVDFVDFVDFVDFVDFVDFVDF 116

124 ARVYLIDLDLFFFTWVFEAPLENNNGFVKVYKSEPEFLVGEALATPKLPJSL 183
 117 ARVYLIDLDLFFFTWVFEAPLENNNGFVKVYKSEPEFLVGEALATPKLPJSL 138
 184 ADTVEVYKQSPREDFVIVAVTDDGDLV-----FLAKDQKRPFTFVY 235
 139 ADTVEVYKQSPREDFVIVAVTDDGDLV-----FLAKDQKRPFTFVY 197
 236 VYVSPDRIIVGNWNNHFWPVLLEBARLGLKIDTGVGASPTTSVGH-----VSPQSL 292
 198 IREKDDVITITNGSDPLPVVRAKGLIKLILGSDG-GSEFGQGRGLDKATVEIKRI 256
 293 NVLDVYAEWMPRIKIKSEVAVYGVWKSKEVRIINWISIPDWDPKPGLLQFAR 352
 257 HDPLHIVERTIMPLTITLLEAVTAEI-GAPKGVTAH--EIAEMTGLGELVAVYS 313
 353 DVAVATYGLAEKLFALQSLVTVGLDQVAVSGLVETLIRAFKCKELVAVNVE 412
 314 EDVAVATYGLAEKLFALQSLVTVGLDQVAVSGLVETLIRAFKCKELVAVNVE 373
 413 REP-----FTTGAIVLEPLAGNHNIAVLPDSFNMIMIKYVNDPLTVRGSEKG 466
 374 ERYEYERLREISAGCTVVFSPKMGSLVSDLPSPISLITINVSPLDRE----- 427
 466 CCQCE-----APVGVHFRCPGFKTVLELLEKRVKVMKCKVPDSEVRLDQEK 523
 428 -QCEVDAVAPVHFRCPGFKTVLELLEKRVKVMKCKVPDSEVRLDQEK 485
 524 AKLVANASTVGMHSCAFYCRCAKAVTANGSHLR-TAINAKIKLVIGVDTDSI 582
 486 AKLVANASTVGMHSCAFYCRCAKAVTANGSHLR-TAINAKIKLVIGVDTDSI 545
 583 FVTY-----DPEVVE-----NFKIKKEELG--FEIKLVKVLFFTBKRVVAGLDDRI 633
 546 YATIPGKPFEEIKVLEPEVHINAKLPOLLELEYEGFVGRGV-TKKYALIDSEKI 604
 634 DVGPEAVGDKCELAEVQVKEIVKATSEVNAVENVRKIVKLEKGVPEKLVIM 693
 605 ITRGLVVRDSEIATETQAKVLEILKGNVENKIVKVEIKLSWETIPEKLVY 664
 694 KTLSEKLVETTPAHVAAKMSAGVYSGDKIVGVIVKVGZGRISORAPYFWK----- 751
 665 EQITRLEPVKATGVHVAVAAKMGVYKVGKGVGTIVGLRDPISKRA-----ILASEP 721
 752 DP-SQIDTVITQITPAARSLGVYKELKASVTAAGTCTVDFVAKSK 803
 722 DPKVYDAVYIENQVLAVLAEVYKELKASVTAAGTCTVDFVAKSK 775
 RESULT 7
 Q959H6 PRELIMINARY; PRT; 775 AA.
 ID Q959H6
 AC Q959H6_2001 (TRENBLrel. 15, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE DNA polymerase (EC 2.7.7.7).
 OS Archaea: Euryarchaeota.
 OC Archaea: Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 SK NCBI_Taxid:74610;
 RP SEQUENCE FROM N.A.
 RC STRAIN=AL546;
 RA Querrelon J., Cambon M.A., Lesongeur F., Barbier G.;
 RT Thermococcales taxonomy and phylogeny based on the comparative use of
 KL submitted, 486-235 rRNA intergenic spacer and family B DNA polymerase
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 CC -/- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N DIPHOSPHATE
 CC -/- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.

FNHL: A2250335, GNC12849.1, --
 DR HSP: P56689; LTGO.
 DR InterPro: IPRO06172; DNA_Pol_B.
 DR InterPro: IPRO06134; DNA_Pol_B.dom.
 DR InterPro: IPRO06133; DNA_Pol_B.exo.
 DR InterPro: IPRO06132; DNA_Pol_B.dom.
 DR Pfam: PF00136; DNA_Pol_B.1.
 DR Pfam: PF03104; DNA_Pol_B.exo.1.
 DR PRINTS: PR00106; DNAPOB.
 DR TIGRFAM: TIGRFAM00459; Pol2.1.
 DR TIGRFAM: TIGRFAM00460; Pol2.1.
 DR PROSITE: PS00116; DNA_POLYMERASE_B.1.
 DR DNA replication; DNA-Binding; DNA-directed DNA polymerase;
 DR Transference. 75 aa; 30417 Wt; 633F932DBE6C73 CRe54;
 QY SEQUENCE 75 aa; 30417 Wt; 633F932DBE6C73 CRe54;
 Query Match 30.2%; Score 1264; DB 1; Length 775;
 Best Local Similarity 36.5%; Pred. No. 2.1e-78;
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 QY 8 VLDSEYVVGKPEVINGIANGSERVIVDIFSRFPYFALLAGADPQV---AQIR 63
 Db 2 TLADYITDEGKPIIFK-KENGFEVDFYDNRFPYFALLADKSDIQIDVKKATASRG 60
 QY 64 ALADSPISPIGVEDHDEGPRFARVETKLVPEAVSEVLEVDQVDEKATVAF 123
 Db 2 ALADSPISPIGVEDHDEGPRFARVETKLVPEAVSEVLEVDQVDEKATVAF 123
 QY 61 KIVR---IVQVKKVKKKIPRIEYKWKIVFEPHQPVAIDKIEHPAVVDFIDFF 116
 Db 2 KIVR---IVQVKKVKKKIPRIEYKWKIVFEPHQPVAIDKIEHPAVVDFIDFF 116
 QY 124 NKWYIDHLPFFYTVFVPELEKNGFRVDYKIVLSRPPKAGENALVTKLRIL 183
 Db 2 NKWYIDHLPFFYTVFVPELEKNGFRVDYKIVLSRPPKAGENALVTKLRIL 183
 QY 117 AKYIDIMGLI-----PMED- 138
 Db 2 AKYIDIMGLI-----PMED- 138
 QY 184 NDTIVSGSGFRRPRPVYANKVDQGVL-----FIAGGDQKPIREFVEY 235
 Db 2 NDTIVSGSGFRRPRPVYANKVDQGVL-----FIAGGDQKPIREFVEY 235
 QY 139 ADITLTHESG-SFANGKPIIMSVADGKAVITKWKVLPVSVESRHEKFLK 197
 Db 2 ADITLTHESG-SFANGKPIIMSVADGKAVITKWKVLPVSVESRHEKFLK 197
 QY 226 WKYDDPDIIVGNNNHFPYLLRARIKGLKIDTVREVAEPTSTVHG---NSVPEL 292
 Db 2 WKYDDPDIIVGNNNHFPYLLRARIKGLKIDTVREVAEPTSTVHG---NSVPEL 292
 QY 198 IRKDDPDIIVGNNSFLPVNKKKGLKLPLESD-GSRHQRQRLDQWVINGRI 256
 Db 2 IRKDDPDIIVGNNSFLPVNKKKGLKLPLESD-GSRHQRQRLDQWVINGRI 256
 QY 293 INDVLDVAEMPEFKTILEVAVYLGWKKSERVIVNHWEIPYDDPKRPALLQVAF 352
 Db 2 INDVLDVAEMPEFKTILEVAVYLGWKKSERVIVNHWEIPYDDPKRPALLQVAF 352
 QY 257 NPDIVHIVTINPTIYETLALF--FORPKRYTH--ELAEATMAGVAKVSM 313
 Db 2 NPDIVHIVTINPTIYETLALF--FORPKRYTH--ELAEATMAGVAKVSM 313
 QY 353 DVRYATYGLAKILPAISLVYGLPDQVAGSGVLEWLTIRAAQFQKMLVNRVE 412
 Db 2 DVRYATYGLAKILPAISLVYGLPDQVAGSGVLEWLTIRAAQFQKMLVNRVE 412
 QY 314 EKAYTILGREGPFEMASLWQVLPQVDSVSSGTCGVLYLKAIVENALNAPKP 373
 Db 2 EKAYTILGREGPFEMASLWQVLPQVDSVSSGTCGVLYLKAIVENALNAPKP 373
 QY 413 RPS---ETRGALVLEPLRGVHMINVLPSSWYNTIKIKVYVQPTLVPRQKCE 466
 Db 2 RPS---ETRGALVLEPLRGVHMINVLPSSWYNTIKIKVYVQPTLVPRQKCE 466
 QY 374 RRYERLRHSAGTVYSEKPGKMEGLVDSFSLPSTIIITHNSDPTLNR--- 427
 Db 2 RRYERLRHSAGTVYSEKPGKMEGLVDSFSLPSTIIITHNSDPTLNR--- 427
 QY 467 GCGD---APEVHRPCCPCEKPTVLELLERLAKKMKKYPDPPYLLERQK 523
 Db 2 GCGD---APEVHRPCCPCEKPTVLELLERLAKKMKKYPDPPYLLERQK 523
 QY 428 -GCEYDVAPVEKCEKQCFEFTPSLLKLLDDEGQETKMKKA-SKDPTEKMLDQ 485
 Db 2 -GCEYDVAPVEKCEKQCFEFTPSLLKLLDDEGQETKMKKA-SKDPTEKMLDQ 485
 QY 524 MVLNANSGVNSGSGKSCQKAVYANSHSLR-PAINAKGLKLVYVQPSL 582
 Db 2 MVLNANSGVNSGSGKSCQKAVYANSHSLR-PAINAKGLKLVYVQPSL 582
 QY 486 MVLNANSGVNSGSGKSCQKAVYANSHSLR-PAINAKGLKLVYVQPSL 545
 Db 2 MVLNANSGVNSGSGKSCQKAVYANSHSLR-PAINAKGLKLVYVQPSL 545
 QY 583 FVTY---DPKVE---NFKIKIIEELG--FEIKLVKIVYKLETFEAKQVALLDEQRI 633
 Db 2 FVTY---DPKVE---NFKIKIIEELG--FEIKLVKIVYKLETFEAKQVALLDEQRI 633
 QY 546 YATIPGAPPEIKKALFVYINAKLPCLLELYEYVYVQPTV-TKRLADVIR 604
 Db 2 YATIPGAPPEIKKALFVYINAKLPCLLELYEYVYVQPTV-TKRLADVIR 604
 QY 634 DYGFAQVCEKAKVQKVEIVKTSSEVNAKAVYKVLVKELEGKVPLEKLV 693
 Db 2 DYGFAQVCEKAKVQKVEIVKTSSEVNAKAVYKVLVKELEGKVPLEKLV 693
 QY 605 TNGDLVTRNDSALNQVNLQNLGNGVETAKVIMETVLSKXITPEKLV 664
 Db 2 TNGDLVTRNDSALNQVNLQNLGNGVETAKVIMETVLSKXITPEKLV 664
 QY 694 KTVLSKRLYEYTAHVAAKELANGVYSGDKGVTVVGGSGISQAMPYKVK-- 751
 Db 2 KTVLSKRLYEYTAHVAAKELANGVYSGDKGVTVVGGSGISQAMPYKVK-- 751
 QY 755 QPTP-HEYTAQVAVAKVAKVAKVPMQVTVTVAGQDQVISEKA---ILASEP 721
 Db 2 QPTP-HEYTAQVAVAKVAKVAKVPMQVTVTVAGQDQVISEKA---ILASEP 721
 QY 762 DP--SDIVDTYDQVHLPAINRIGVQPTIKTKVANSQVQPTIDPELAKSE 803
 Db 2 DP--SDIVDTYDQVHLPAINRIGVQPTIKTKVANSQVQPTIDPELAKSE 803


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RL EMBL: 420,563-573 (2002)
DR EMBL: AK088310; BAC00278.1; -.
SQ SEQUENCE 1105 AA; 123776 MW; 20323377DD472281 CRC64;

Query Match
Best Local Similarity 17.9%; Score 744.5; DB 11; Length 1105;
Matches 246; Conservative 153; Mismatches 319; Indels 165; Gaps 33;

QY 20 PQTIVGIAKNGERVLDISFRVYVALLAFGADQVQQRIR---ALSPPK-----69
Db 121 PLIRAFVQVDFGSEVCHIGCFANFYVTPAFGAGHSELSQELNAAISDQSGKEL 180
QY 221 -----EGKDDKPIREYVYVQVDPDIIVGNHNPDPILLRA-----261
QY 356 RCPALPGAKVQSTREUL---LQNAWDTPLAVQVITQINQDFLILISBAQALY 413
QY 262 -----RLIGLGLV-----TRRGAFTSVHGVHGVGLAVLDVYAEEMPEIKI 308
QY 414 DRFFPLQVLTGASIMDESSVQSGVGRDSKY---ISMVGVQMDQLVGLREKHA 469
QY 309 KSLEVA-EYLGVNKSSEVILNMWIDPDWDPKRFLQYARDVR---ATYGLAEK 364
QY 470 YTLMAVSHPFGSDQVQHQI---ITD-----LONGBOTRRRLAYCLQDA 514
QY 365 TLPPA-----TQSVYVGLQVQVGVNSVGLFELVILRAAFKQELVNVYER 413
QY 515 PLIRARLERLVLMNVVYVAVVQVGLTLLTQVQGVKVSQALLQVQGLLAPVYKE 574
QY 414 PREYVGAIVLEPLGAEH-NIANVQSDSSVNTKYNVQDTIVRPG---EKGGCCOH 470
QY 575 GQEDVGTAVTPELAGTVQVITADPSLSYFSIMAHNLCTYTLAPQVQALG---629
QY 471 EAPR-----VQHPRCPGCFKTVLELLERLVKVAWKKVYKPSPEVLLD 519
QY 630 LKPDFTKTTGDFEVSSEVK---GLPQLELLSNARKAAELAQ-ETDPLRQVLD 685
QY 520 ESKQALNTAVNQHGVNSKAWYCRKCAKNTAVGHELLRTATNANK-----L 570
QY 686 GQALAKYVNSVYGTGAQVGLQCLIEISQVTFGQAKTQVLSKNTYVNGDA 745
QY 571 GLNVTGHTDLSLVYTPDKRNFYIKELGEL-----EYLKTVKPLFTFEAK 621
QY 746 NAKTVAGTQDSVGVGSSVAVASGLREANVNSHPISRLERFAYFP-YLLISK 804
QY 622 KYVGLAEOR-----ITVGFARQVQCEAFVQVTVKEI VIKTSVKNVAVYER 864
QY 805 NAKVLTSSRSDAHQDQKGLAEVREDCQVYVNLVTSLSLRIMQDPQVAVR 970
QY 676 IVYELBECKVFPEKLVNKLISRLREYTTAPVVAAGM---LEAGVVEPQDQIGVY 733
QY 865 VLSQDLQNDISQVITKELITADNATQVQKQVLAELAKNKKDQSGSLQDQVFTY 924
QY 734 V---KGGGSIQRAMPYVQPSQIDVYVQDQIIPAAKI 773
QY 925 IGANVGVAAYKSEDPFLVLEHSLDIPDTYQLQGLQAPLHAI 967

RESULT 15
Q91V70 PRELIMINARY; PRT; 1105 AA.
ID Q91V70

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Db 575 GSEDYGTATVIEPLAGYDVIATIDFSSLYPSIWAUNLCVTTLLRPGAKQLG----- 629
Qy 471 EAPB-----VHRFRCPGPFKTVLLELLELRVRAWMKYPPSPETRLID 519
Db 530 LARDEFIKTQDEFVSSVR--GLLPQLLELLLSRRRBAUQLAQ-ETDLARQYLD 685
Qy 520 ERQALKYLANASYGWMGSGARWYCECAAVTANGHLLRTAINIARK-----L 570
Db 686 GROLALKYNSYVGTGAQVGLCLLISQSVTGFQGMHKTQKLVESKYTVENGIDA 745
Qy 571 GLKVIYGOTSLFYIDPEKVENFIKKEELG-----EIKLEKYKELFFTEAK 621
Db 746 NAKVYVGTDSVRCFVGSVAEASIGREANWSSHPSPIRLEFEKYTFP-ILLISK 804
Qy 622 KRYAGLLEDGR-----IDVGFVAVRGDCLEAREVOTKVELVLTSEVNMAVEYRK 675
Db 805 KRYAGLLFSRDDHMDCKGLEAVRDMCPVANLVTSIRLLVDKDPDGNVAHAXD 864
Qy 676 IYKLESEKYPTEKLVMTKLSKRLVEYTTAPHVVAKEN--LSNGYVRSQDKGTVI 733
Db 865 VISDLLCRIDISQVITKELTRAAADYAGQAHVELAEHRMRKDDSGAPSLDRVPTVI 924
Qy 734 V--KGGGRISGRAPYFNVKPSQIDVTYVVDHJITPAURI 773
Db 925 IGAKGVAAVMSSEDFVLEHSLPTPTQYLEQQAKPLAI 967

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Search completed: November 25, 2003, 14:59:52
 Job time : 47 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: November 25, 2003, 14:52:23 ; Search time 48 Seconds
 (without database updates/sec
 2655.365 Million cell updates/sec)

US-10-034-849-2

Title:

Perfect score: 4188

Sequence: 1 MTEVFVFLVLSIEVGVKEP.....LKASNTQKRLFFWLAKEKH 803

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107863 seps. 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_13Jun03.*

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 2: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1981.DAT.*
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 23: /SIDSI/gcgdata/geneseq/geneseq-emb/AA2002.DAT.*
 24: /SIDSI/gcgdata/geneseq/geneseq-emb/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4188	100.0	803	20	AAV00936
2	4188	100.0	803	23	AA822118
3	4188	100.0	803	24	AA822115
4	4188	100.0	803	24	AA822115
5	4188	100.0	803	24	AA822112
6	4164	99.4	803	24	AA822119
7	4164	99.4	803	24	AA822116
8	4164	99.4	803	24	AA822113
9	4122	96.4	799	23	AA822120

Pyrodictum occult
 P. occultum DNA po
 P. occultum DNA po
 Pyrobaculum AF0497
 Pyrobaculum AF0497
 A. fulgidus AF0497
 A. fulgidus AF0497
 A. lithophilus AF0497
 A. lithophilus AF0497
 Archaeoglobus lith
 Archaeoglobus lith
 Archaeoglobus therm
 P. kodakarensis K
 P. kodakarensis K
 Heat-resistant Pfu
 Heat-resistant Pfu
 Heat-resistant Pfu
 Heat-resistant Pfu
 Pyrococcus kodak
 P. kodakarensis K
 P. kodakarensis K
 Mutant KOD DNA pol
 Mutant KOD DNA pol
 P. kodakarensis K
 Heat-resistant Pfu
 Heat-resistant Pfu
 T. profundus therm
 T. profundus therm
 Heat-resistant DNA
 Heat-resistant DNA
 Pyrococcus furiosu
 Pyrococcus furiosu
 Wild-type P. furio
 P. furiosus (Pfu)
 P. furiosus DNA po
 P. furiosus DNA po
 Thermococcus goiso
 Thermococcus goiso
 Mature DNA polymer
 KOD1 thermostable
 KOD1 thermostable
 Mutant KOD DNA pol
 Mutant KOD DNA pol
 Mutant KOD DNA pol

ALIGNMENTS

RESULT 1

AAV00936
 XX AAV00936 standard; Protein; 803 aa.
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 XX AC
 XX AC 02-JUN-1999 (first entry)
 XX DE
 XX DE P. furarius DNA polymerase 1P2 protein sequence.
 XX KW
 XX KW DNA polymerase; thermophilic bacteria; DNA synthesis.
 XX KW
 XX KW Pyrobaculum furarius.
 XX OS
 XX OS WO9007837-A1.
 XX FN
 XX FN 18-FEB-1999.
 XX PF
 XX PF 06-AUG-1998; 98MO-US17152.
 XX XX
 XX XX 06-AUG-1997; 97US-0907166.
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 XX XX Callen W, Mathur EJ;
 XX XX NPSB; 1999-180490/15.
 XX XX DR
 XX XX DR N-PSB; AA827283.
 XX XX
 XX XX DNA polymerases from extremely thermophilic bacteria - useful for
 XX XX DNA synthesis

Claim 1; Fig 2; 72pp; English.

This sequence is a DNA polymerase of the invention, that was isolated from a thermophilic bacteria. The polymerases are used in DNA synthesis and as immunogens to raise antibodies. Fragments of the DNA encoding the polymerases are used as probes to isolate related or full-length sequences and to produce the recombinant polymerases. The polymerase catalyze DNA synthesis by the addition of deoxynucleotides to a growing strand of DNA. The polymerases are used as a template. The polymerases have optimum activity at over 60 deg. C and can renature and regain activity after exposure to temperatures above 70 deg. C.

XX	Sequence	803 AA;
XX	Query Match	100.0%; Score 4188; DB 20; Length 803;
XX	Best Local Similarity	100.0%; Pred. No. 0;
XX	Matches	803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	MTWVFTVLSSTVEVGGKFPVFIWGLANGSERVILDSFRFPVYALLAGADPKVQAQ 60
Db	1	MTWVFTVLSSTVEVGGKFPVFIWGLANGSERVILDSFRFPVYALLAGADPKVQAQ 60
Qy	61	RTALRGSRKSPHIGVEDDKRFPGRPRVRLRTVPEAVRELVGVGVLEAD 120
Db	61	RTALRGSRKSPHIGVEDDKRFPGRPRVRLRTVPEAVRELVGVGVLEAD 120
Qy	121	IFAPMAYTLDHDLFPFTVTVVEAPELNGGFRVDKTVLSEAPPLVGEALPTKLPUL 180
Db	121	IFAPMAYTLDHDLFPFTVTVVEAPELNGGFRVDKTVLSEAPPLVGEALPTKLPUL 180
Qy	181	RTLAFDIEVYSQSGSRPRDPVIVAVKTDGQVLFIAEGDKRPFVEFVRYD 240
Db	181	RTLAFDIEVYSQSGSRPRDPVIVAVKTDGQVLFIAEGDKRPFVEFVRYD 240
Qy	241	PDIVGVNNHDFPVLARARLTGIDVTRVGAERTTSVGHVSFGRLAVLYDA 300
Db	241	PDIVGVNNHDFPVLARARLTGIDVTRVGAERTTSVGHVSFGRLAVLYDA 300
Qy	301	ESMPEKTKLESEVAYLVGVKSGSERVILNNMETPDVNDPKPELLOVARDVATYG 360
Db	301	ESMPEKTKLESEVAYLVGVKSGSERVILNNMETPDVNDPKPELLOVARDVATYG 360
Qy	361	IAKMLKPLFQVTSVGLPDQGVANGSVFHEMLVILAFAPFMKLVNRPVPEETYG 420
Db	361	IAKMLKPLFQVTSVGLPDQGVANGSVFHEMLVILAFAPFMKLVNRPVPEETYG 420
Qy	421	ATVNSPKGKHENIAVNSRSPKVMKIVGQDPLVYRCHQKCGGCVASVGRER 480
Db	421	ATVNSPKGKHENIAVNSRSPKVMKIVGQDPLVYRCHQKCGGCVASVGRER 480
Qy	481	ICDPGKFTVLELLLEKLVLEAMKCPDPSPTFLIDRKNKALVANKSVGNSG 540
Db	481	ICDPGKFTVLELLLEKLVLEAMKCPDPSPTFLIDRKNKALVANKSVGNSG 540
Qy	541	ARYTCRCNAVTAHGRLLTAIMIARKLGANTIGTDSIFPTDPEKNVFIKLE 600
Db	541	ARYTCRCNAVTAHGRLLTAIMIARKLGANTIGTDSIFPTDPEKNVFIKLE 600
Qy	601	ELAGFIEKLVKELFEACKYVAGLLEEDRGDITVGEAVNGCCLAEKQVTVLV 660
Db	601	ELAGFIEKLVKELFEACKYVAGLLEEDRGDITVGEAVNGCCLAEKQVTVLV 660
Qy	661	LKTSVNAKVEVVKVLEEGVPEFKVTKLSKLEETVTAAPHVAARMISAG 720
Db	661	LKTSVNAKVEVVKVLEEGVPEFKVTKLSKLEETVTAAPHVAARMISAG 720
Qy	721	YVSGDKIGTVVNGGRISORAPYFMWDPSQIDITVVDHQIIPAAIRLIGTGT 780
Db	721	YVSGDKIGTVVNGGRISORAPYFMWDPSQIDITVVDHQIIPAAIRLIGTGT 780
Qy	781	EKKGLASATGKTLFPLAKSEK 803

Claim 1; Fig 2; 72pp; English.

This sequence is a DNA polymerase of the invention, that was isolated from a thermophilic bacteria. The polymerases are used in DNA synthesis and as immunogens to raise antibodies. Fragments of the DNA encoding the polymerases are used as probes to isolate related or full-length sequences and to produce the recombinant polymerases. The polymerase catalyze DNA synthesis by the addition of deoxynucleotides to a growing strand of DNA. The polymerases are used as a template. The polymerases have optimum activity at over 60 deg. C and can renature and regain activity after exposure to temperatures above 70 deg. C.

XX	Sequence	803 AA;
XX	Query Match	100.0%; Score 4188; DB 23; Length 803;
XX	Best Local Similarity	100.0%; Pred. No. 0;
XX	Matches	803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	MTWVFTVLSSTVEVGGKFPVFIWGLANGSERVILDSFRFPVYALLAGADPKVQAQ 60
Db	1	MTWVFTVLSSTVEVGGKFPVFIWGLANGSERVILDSFRFPVYALLAGADPKVQAQ 60
Qy	61	RTALRGSRKSPHIGVEDDKRFPGRPRVRLRTVPEAVRELVGVGVLEAD 120
Db	61	RTALRGSRKSPHIGVEDDKRFPGRPRVRLRTVPEAVRELVGVGVLEAD 120
Qy	121	IFAPMAYTLDHDLFPFTVTVVEAPELNGGFRVDKTVLSEAPPLVGEALPTKLPUL 180
Db	121	IFAPMAYTLDHDLFPFTVTVVEAPELNGGFRVDKTVLSEAPPLVGEALPTKLPUL 180
Qy	181	RTLAFDIEVYSQSGSRPRDPVIVAVKTDGQVLFIAEGDKRPFVEFVRYD 240
Db	181	RTLAFDIEVYSQSGSRPRDPVIVAVKTDGQVLFIAEGDKRPFVEFVRYD 240
Qy	241	PDIVGVNNHDFPVLARARLTGIDVTRVGAERTTSVGHVSFGRLAVLYDA 300
Db	241	PDIVGVNNHDFPVLARARLTGIDVTRVGAERTTSVGHVSFGRLAVLYDA 300

Claim 1; Fig 2; 72pp; English.

This sequence is a DNA polymerase of the invention, that was isolated from a thermophilic bacteria. The polymerases are used in DNA synthesis and as immunogens to raise antibodies. Fragments of the DNA encoding the polymerases are used as probes to isolate related or full-length sequences and to produce the recombinant polymerases. The polymerase catalyze DNA synthesis by the addition of deoxynucleotides to a growing strand of DNA. The polymerases are used as a template. The polymerases have optimum activity at over 60 deg. C and can renature and regain activity after exposure to temperatures above 70 deg. C.

XX	Sequence	803 AA;
XX	Query Match	100.0%; Score 4188; DB 23; Length 803;
XX	Best Local Similarity	100.0%; Pred. No. 0;
XX	Matches	803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	MTWVFTVLSSTVEVGGKFPVFIWGLANGSERVILDSFRFPVYALLAGADPKVQAQ 60
Db	1	MTWVFTVLSSTVEVGGKFPVFIWGLANGSERVILDSFRFPVYALLAGADPKVQAQ 60
Qy	61	RTALRGSRKSPHIGVEDDKRFPGRPRVRLRTVPEAVRELVGVGVLEAD 120
Db	61	RTALRGSRKSPHIGVEDDKRFPGRPRVRLRTVPEAVRELVGVGVLEAD 120
Qy	121	IFAPMAYTLDHDLFPFTVTVVEAPELNGGFRVDKTVLSEAPPLVGEALPTKLPUL 180
Db	121	IFAPMAYTLDHDLFPFTVTVVEAPELNGGFRVDKTVLSEAPPLVGEALPTKLPUL 180
Qy	181	RTLAFDIEVYSQSGSRPRDPVIVAVKTDGQVLFIAEGDKRPFVEFVRYD 240
Db	181	RTLAFDIEVYSQSGSRPRDPVIVAVKTDGQVLFIAEGDKRPFVEFVRYD 240
Qy	241	PDIVGVNNHDFPVLARARLTGIDVTRVGAERTTSVGHVSFGRLAVLYDA 300
Db	241	PDIVGVNNHDFPVLARARLTGIDVTRVGAERTTSVGHVSFGRLAVLYDA 300

Db 241 PDIIYVNNHDPFTLLPRLALIGLKLDTVRVCAEPTTSVGHNSVPGRLNVDYDA 300
 Qy 301 BEWPKIKSLSEVARYGVNKSSEVIVNWEIDPDMDPKRLLQYADDVYATG 360
 Db 301 BEWPKIKSLSEVARYGVNKSSEVIVNWEIDPDMDPKRLLQYADDVYATG 360
 Qy 361 LAKLILFPAQLSTVYGLPDQGVMSVGFRLNLTAAFPKMLVKNVVERPEETG 420
 Db 361 LAKLILFPAQLSTVYGLPDQGVMSVGFRLNLTAAFPKMLVKNVVERPEETG 420
 Qy 421 AVILBPGRVHENTAVLDFSSPMYIKINVGDTVFGKCGCCVCEVAVRFR 480
 Db 421 AVILBPGRVHENTAVLDFSSPMYIKINVGDTVFGKCGCCVCEVAVRFR 480
 Qy 481 RCPGPFVTLERLLERKVRBMKYPPOSPEYLLDEROKALVLANASYGMHGS 540
 Db 481 RCPGPFVTLERLLERKVRBMKYPPOSPEYLLDEROKALVLANASYGMHGS 540
 Qy 541 ARWYCRCKAVATAGRHILFTATNARKLGLKVIYDTSLSFTVYDPEKVFILKE 600
 Db 541 ARWYCRCKAVATAGRHILFTATNARKLGLKVIYDTSLSFTVYDPEKVFILKE 600
 Qy 601 ELGSLVYKPKLAFETKAGVYAGLLENDRIYVFENWGCWCELAKEVQYKVEIV 660
 Db 601 ELGSLVYKPKLAFETKAGVYAGLLENDRIYVFENWGCWCELAKEVQYKVEIV 660
 Qy 661 LKTSSEWKAIVEYKALVLEEGSVPIKNTKLEAEVYETEARVYAKWLSAG 720
 Db 661 LKTSSEWKAIVEYKALVLEEGSVPIKNTKLEAEVYETEARVYAKWLSAG 720
 Qy 721 YNSFGKQGVTVWGGRIISQANVYVWVQSDIVYVWVHSDIIPAMALIGVGT 780
 Db 721 YNSFGKQGVTVWGGRIISQANVYVWVQSDIVYVWVHSDIIPAMALIGVGT 780
 Qy 781 ENKLKASATGKTLDPFAKSK 803
 Db 781 ENKLKASATGKTLDPFAKSK 803

RESULT 3

ID: 0379155; Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Accession: US0201312243-1A1.

Novel DNA polymerases having increased activity and stability at increased pH and temperature, useful for DNA sequencing, amplification and incorporating non-natural nucleotides or nucleotide analogs - Claim 42, Fig 1; 81pp; English.

This invention relates to a novel purified polypeptide derived from a host organism, which has a thermostable DNA polymerase activity. The protein of the invention is useful for catalysing the formation or repair of a nucleic acid sequence, for comparing a sequence to a reference sequence and for identifying polymorphisms. The nucleic acid sequence of the invention is useful for identifying polymorphisms and in an amplification process of a double-stranded DNA molecule. The nucleotide sequence is also useful for incorporating non-natural nucleotides or its analogues into a DNA molecule, by contacting a polypeptide encoded by the nucleic acid sequence of the invention with a nucleic acid sequence. The nucleotides which may be used for this are inosine, 2-aminopurine or 5-methylcytosine. A nucleic acid probe derived from the nucleic acid sequence of the invention is useful in chromosome walking procedures to identify clones containing genomic sequences of the invention. Such methods allow the isolation of genes which encode additional proteins from the host organism. The polymerases of the invention have increased activity and stability at increased pH and temperature, and high processivity. The polymerases of the invention are useful for amplifying DNA and for incorporating non-natural nucleotides or nucleotide analogs into a DNA molecule. The protein of the invention.

Sequence 803 AA;

Query Match 100.0%; Score 4188; DB 24; Length 803;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEVVFVLLSSVTVGKPEQVILITANGSERVILDRSEPFVYALLAGADPKQVQA 60
 Db 1 MTEVVFVLLSSVTVGKPEQVILITANGSERVILDRSEPFVYALLAGADPKQVQA 60
 Qy 61 ETALSRKSPGIIQTDKPKYKQFPRVLIETVLPAAVREYLVNNGVDEYDLEAD 120
 Db 61 ETALSRKSPGIIQTDKPKYKQFPRVLIETVLPAAVREYLVNNGVDEYDLEAD 120
 Qy 121 TRNMYVLTIDGDPFTVYHRAEPLKNGKGVYVYLVKSRPEPAALPTKLPOL 180
 Db 121 TRNMYVLTIDGDPFTVYHRAEPLKNGKGVYVYLVKSRPEPAALPTKLPOL 180
 Qy 181 KILADTEVYSKQSPREDFVIAVKTDDGAVLITFAEVRVDELVNNGVDEYDLEAD 240
 Db 181 KILADTEVYSKQSPREDFVIAVKTDDGAVLITFAEVRVDELVNNGVDEYDLEAD 240
 Qy 241 PDIIYVNNHDPFTLLPRLALIGLKLDTVRVCAEPTTSVGHNSVPGRLNVDYDA 300
 Db 241 PDIIYVNNHDPFTLLPRLALIGLKLDTVRVCAEPTTSVGHNSVPGRLNVDYDA 300
 Qy 301 BEWPKIKSLSEVARYGVNKSSEVIVNWEIDPDMDPKRLLQYADDVYATG 360
 Db 301 BEWPKIKSLSEVARYGVNKSSEVIVNWEIDPDMDPKRLLQYADDVYATG 360
 Qy 361 LAKLILFPAQLSTVYGLPDQGVMSVGFRLNLTAAFPKMLVKNVVERPEETG 420
 Db 361 LAKLILFPAQLSTVYGLPDQGVMSVGFRLNLTAAFPKMLVKNVVERPEETG 420
 Qy 421 AVILBPGRVHENTAVLDFSSPMYIKINVGDTVFGKCGCCVCEVAVRFR 480
 Db 421 AVILBPGRVHENTAVLDFSSPMYIKINVGDTVFGKCGCCVCEVAVRFR 480
 Qy 481 RCPGPFVTLERLLERKVRBMKYPPOSPEYLLDEROKALVLANASYGMHGS 540
 Db 481 RCPGPFVTLERLLERKVRBMKYPPOSPEYLLDEROKALVLANASYGMHGS 540
 Qy 541 ARWYCRCKAVATAGRHILFTATNARKLGLKVIYDTSLSFTVYDPEKVFILKE 600
 Db 541 ARWYCRCKAVATAGRHILFTATNARKLGLKVIYDTSLSFTVYDPEKVFILKE 600

XX 06-SEP-2000; 2000US-0656309.
 XX (DIVE-) DIVERGA CORP.
 XX Callen M, Nachur EJ, Short JW;
 XX WPI; 2002-362247/39.
 XX N-PSDB; AAD55186.
 XX New thermostable polymerase useful for sequencing DNA, amplifying
 XX double stranded DNA, or incorporating a non-natural nucleotide or a
 XX nucleotide analog into a DNA molecule -
 XX Claim 42; Fig 11; 16pp; English.
 XX The invention relates to thermostable DNA polymerases having high
 XX temperature polymerase activity, such as the ability to incorporate
 XX Pyrophosphate (PPi) into the DNA sequence, and to encode such polymerases.
 XX Polynucleotide sequences are provided for the formation or repair of a
 XX polynucleotide sequence and for modifying small molecules. They are also
 XX useful for sequencing DNA molecules, for preparing cDNA from non-
 XX amplifying double stranded DNA, and for incorporating a non-natural
 XX nucleotide or nucleotide analog into a DNA molecule. The
 XX present sequence is *Pyrobolus fumariae* DNA polymerase.
 XX Sequence 803 AA;
 XX Query Match 99.4%; Score 4164; DB 23; Length 803;
 XX Best Local Similarity 99.3%; Pred. No. 0;
 XX Matches 797; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1 MTEVETVLDSSVEYCKSPQVINGIAENGSRVULIDRSFPFYFALLAGDAPQVAAQ 60
 XX DB 1 MTEVETVLDSSVEYCKSPQVINGIAENGSRVULIDRSFPFYFALLAGDAPQVAAQ 60
 XX
 XX 61 RTALSRKSPSLIGEDVDYKGRPRVLRITVLPFAVREYELVYGVGVDEAD 120
 XX QY 61 RTALSRKSPSLIGEDVDYKGRPRVLRITVLPFAVREYELVYGVGVDEAD 120
 XX DB 61 RTALSRKSPSLIGEDVDYKGRPRVLRITVLPFAVREYELVYGVGVDEAD 120
 XX
 XX 121 TQPMNVI TDGLFDPFTVYVFAELENVGVFVDCYLVKSPPELYGKALPTKPLD 180
 XX QY 121 TQPMNVI TDGLFDPFTVYVFAELENVGVFVDCYLVKSPPELYGKALPTKPLD 180
 XX DB 121 TQPMNVI TDGLFDPFTVYVFAELENVGVFVDCYLVKSPPELYGKALPTKPLD 180
 XX
 XX 181 RLAFDITVYKSGSPRRPVVTVANKTDGDDVFLFAEGDKDGRFPFVGVYVD 240
 XX QY 181 RLAFDITVYKSGSPRRPVVTVANKTDGDDVFLFAEGDKDGRFPFVGVYVD 240
 XX DB 181 RLAFDITVYKSGSPRRPVVTVANKTDGDDVFLFAEGDKDGRFPFVGVYVD 240
 XX
 XX 241 PDLVGNMNTVYVLLARSLGKGVTVAGVSGVGVGVGVGVGVGVGVGVGVGV 300
 XX QY 241 PDLVGNMNTVYVLLARSLGKGVTVAGVSGVGVGVGVGVGVGVGVGVGV 300
 XX DB 241 PDLVGNMNTVYVLLARSLGKGVTVAGVSGVGVGVGVGVGVGVGVGV 300
 XX
 XX 301 EMBEETIKLSSEVATVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 360
 XX QY 301 EMBEETIKLSSEVATVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 360
 XX DB 301 EMBEETIKLSSEVATVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 360
 XX
 XX 361 LAKETIKLPALQVTVGLDQVGMSSVFLRLETLIRAFPMGLVYVNVFPEPTG 420
 XX QY 361 LAKETIKLPALQVTVGLDQVGMSSVFLRLETLIRAFPMGLVYVNVFPEPTG 420
 XX DB 361 LAKETIKLPALQVTVGLDQVGMSSVFLRLETLIRAFPMGLVYVNVFPEPTG 420
 XX
 XX 421 AVLEELPAGVHENVLDSSPHMINKNGGDPFLVRECKGSGCGWAPVDFR 480
 XX QY 421 AVLEELPAGVHENVLDSSPHMINKNGGDPFLVRECKGSGCGWAPVDFR 480
 XX DB 421 AVLEELPAGVHENVLDSSPHMINKNGGDPFLVRECKGSGCGWAPVDFR 480
 XX
 XX 481 RCPGFFPTVLELLERLKVFAEMKVPSPPEYLLDRQKALVYAGVGMSSG 540
 XX QY 481 RCPGFFPTVLELLERLKVFAEMKVPSPPEYLLDRQKALVYAGVGMSSG 540
 XX DB 481 RCPGFFPTVLELLERLKVFAEMKVPSPPEYLLDRQKALVYAGVGMSSG 540
 XX
 XX 541 ARWVCEGNAVYVNSHLLITATINARKGLGVIGTDSLPYDPEKVFNTIKE 600
 XX QY 541 ARWVCEGNAVYVNSHLLITATINARKGLGVIGTDSLPYDPEKVFNTIKE 600
 XX DB 541 ARWVCEGNAVYVNSHLLITATINARKGLGVIGTDSLPYDPEKVFNTIKE 600
 XX
 XX 601 ELGFEITKLVYVKEFTKANKYAGLLDGRIDIVGEAVGVGCWCELAKEVQTVV 660
 XX QY 601 ELGFEITKLVYVKEFTKANKYAGLLDGRIDIVGEAVGVGCWCELAKEVQTVV 660

DB 601 ELGFEITKLVYVKEFTKANKYAGLLDGRIDIVGEAVGVGCWCELAKEVQTVV 660
 QY 661 LKTSNVAEYVVKVLESEKGPYTERKLVTKWLSQRLTEYTPAHVVAAKMSUG 720
 DB 661 LKTSNVAEYVVKVLESEKGPYTERKLVTKWLSQRLTEYTPAHVVAAKMSUG 720
 QY 721 YVPSGDQKGVTVYVKGSGRIQSQWAMPYVWQSDQVTVYVDRQITPAALRLILGYGIT 780
 DB 721 YVPSGDQKGVTVYVKGSGRIQSQWAMPYVWQSDQVTVYVDRQITPAALRLILGYGIT 780
 QY 781 EKKLAKASATGQVTEFELAKSKK 803
 DB 781 EKKLAKASATGQVTEFELAKSKK 803
 XX RESUFG 7
 XX ASB73161
 XX ID ASB73161 standard; Protein; 803 AA.
 XX XX ASB73161;
 XX ASB73161;
 XX 08-APR-2003 (first entry)
 XX Aquifex pyrophilus thermostable DNA polymerase protein.
 XX Enzyme; thermostable; DNA polymerase; DNA repair;
 XX polymorphism identification.
 XX Aquifex pyrophilus.
 XX XX Aquifex pyrophilus.
 XX US2002132243-A1.
 XX 19-SEP-2002.
 XX 06-SEP-2001; 2001US-0948369.
 XX 06-AUG-1997; 97US-0907166.
 XX 06-SEP-2000; 2000US-0656309.
 XX (CALL) CALLEN M.
 XX (NACHUR) NACHUR E J.
 XX (SHORT) SHORT J.
 XX Callen M, Nachur EJ, Short J;
 XX WPI; 2002-182285/18.
 XX N-PSDB; AAK14890.
 XX Novel DNA polymerases having increased activity and stability at
 XX increased temperatures, and methods for DNA sequencing, amplification
 XX and incorporating non-natural nucleotides or nucleotide analogs -
 XX Claim 42; Page 49-51; 81pp; English.
 XX This invention relates to a novel purified polypeptide derived from
 XX *Pyrobolus fumariae* which has thermostable DNA polymerase activity. The
 XX protein of the invention is useful for catalyzing the formation or
 XX repair of a nucleic acid sequence, for comparing a second nucleic
 XX acid sequence to a first nucleic acid sequence, for sequencing the nucleic
 XX acid sequence, and in an amplification process of a double-stranded DNA molecule.
 XX The nucleotide sequence is also useful for incorporating non-natural
 XX nucleotides or its analogues into a DNA template in a PCR
 XX amplification reaction. The nucleotides which may be used for this are
 XX deoxythymine, deoxycytosine, deoxyadenine, deoxyguanosine, inosine,
 XX 2-aminopurine or 5-methylcytosine. A nucleic acid probe
 XX derived from the nucleic acid sequence of the invention may be used in
 XX a hybridization assay to detect the presence of a specific coding genomic
 XX sequence located adjacent to a sequence of the gene encoding the DNA
 XX polymerase of the invention. Such methods allow the isolation of
 XX genes which encode additional proteins from the host organisms. The

Db 121 IRFAMRYLIDHDLFFPTVRVTEAEPLNNMGFRVDKVLKVSRRPELYGALPTLDEL 180
 Qy 181 RIALPDIIVSVKSGSPRRDPVTVYAVKTDQDEVRVIAKCDKDRPQIRNRYKVVYD 240
 Db 181 RIALPDIIVSVKSGSPRRDPVTVYAVKTDQDEVRVIAKCDKDRPQIRNRYKVVYD 240
 Qy 241 PDIVGNNHNDPMTLLRRARLIGIKLDVTRVGLPTTIVSHGVSVGVLNVLVDYA 300
 Db 241 PDIVGNNHNDPMTLLRRARLIGIKLDVTRVGLPTTIVSHGVSVGVLNVLVDYA 300
 Qy 301 EMPEIKIKLEVAETLVKMSKSRVINWMEIPDWDPKGKLLQAYADVATG 360
 Db 301 EMPEIKIKLEVAETLVKMSKSRVINWMEIPDWDPKGKLLQAYADVATG 360
 Qy 361 LAEKILPFAIQLSVYGLQDVGMSVGRLEWILIDAEFKSELVPRVVERPEITG 420
 Db 361 LAEKILPFAIQLSVYGLQDVGMSVGRLEWILIDAEFKSELVPRVVERPEITG 420
 Qy 421 AVLEPLAGVHENIADVSSPMYKINIKVGPDLVLRGEGCGEGWEAEVGRFR 480
 Db 421 AVLEPLAGVHENIADVSSPMYKINIKVGPDLVLRGEGCGEGWEAEVGRFR 480
 Qy 481 RCPGFFVTYLLERLELRNVEAKMKYPPDSPEYLLDRQALKVLANSYGVMSG 540
 Db 481 RCPGFFVTYLLERLELRNVEAKMKYPPDSPEYLLDRQALKVLANSYGVMSG 540
 Qy 541 ARWCQECANVTAMGRHLITKINTAKKGLKVIYGDYLSLPTDYSKVPYFKIKE 600
 Db 541 ARWCQECANVTAMGRHLITKINTAKKGLKVIYGDYLSLPTDYSKVPYFKIKE 600
 Qy 601 ELGFEIKLEVVYLLPFTAKYVAGLEQSDRIDVGFENVGWGCWELAKVQVNVIV 660
 Db 601 ELGFEIKLEVVYLLPFTAKYVAGLEQSDRIDVGFENVGWGCWELAKVQVNVIV 660
 Qy 661 LKTSKQKQVYKIVKELSESKQPIKSLVNTKLSLSEKVTSDHGVAKVMSG 720
 Db 661 LKTSKQKQVYKIVKELSESKQPIKSLVNTKLSLSEKVTSDHGVAKVMSG 720
 Qy 721 YVSGDKQKQVYKIVKELSESKQPIKSLVNTKLSLSEKVTSDHGVAKVMSG 780
 Db 721 YVSGDKQKQVYKIVKELSESKQPIKSLVNTKLSLSEKVTSDHGVAKVMSG 780
 Qy 781 EKKKASATQNTLPPFAKSK 803
 Db 781 EKKKASATQNTLPPFAKSK 803

RESUME 9

AAE22120
 ID AAE22120 standard; Protein; 799 AA.

XX AAE22120;

XX AAE22120;

XX 25-JUL-2002 (first entry)

XX Pyrobolus fumaria DNA polymerase consensus sequence.

DE DNA polymerase; thermostable; enzyme.

XX Pyrobolus fumaria.

OS WO200220715-A2.

XX 14-MAR-2002.

XX 06-SEP-2001; 2001NO-28007.

XX 06-SEP-2000; 2000US-0656309.

XX (DIVE-) DIVERSA CORP.

XX Callen W, Mather EJ, Short JN;

XX

DR WP1; 2002-36247/39.

XX New thermostable polymerases useful for sequencing DNA, amplifying
 PT substandard DNA, or incorporating a non-natural nucleotide of a
 PT nucleotide analog into a DNA molecule.

XX Dictionnaire; Fig 11; 16pp; English.

XX The invention relates to thermostable DNA polymerases having high
 CC temperature polymerase activity, such as those derived from
 CC Pyrobolus fumaria and nucleic acid molecules encoding such polymerases.
 CC The invention also relates to methods for sequencing DNA, amplifying
 CC nucleic acid sequence and for modifying small molecules. They are also
 CC useful for sequencing DNA molecules, for preparing cDNA from mRNA, for
 CC amplifying double stranded DNA molecules and for incorporating non-
 CC natural nucleotides or nucleotide analogues into a DNA molecule. The
 CC present sequence is Pyrobolus fumaria DNA polymerase consensus sequence.

XX Sequence 799 AA;

Qy Query Match

Best Local Similarity 98.48; Score 4122; DB 23; Length 799;

Matches 798; Conservative 1; Mismatches 0; Indels 4; Gaps 4;

Qy 1 MTRVAVTLDSSVGVSEVQVTVKINLNSGVGVVIGNSRVRVVALAARQVQAQ 60
 Db 1 MTRVAVTLDSSVGVSEVQVTVKINLNSGVGVVIGNSRVRVVALAARQVQAQ 60
 Qy 61 RIALSPSPSLIGVDKIKYKCFRPRVRLITVLPELVEVRELVVQVDSVLEAD 120
 Db 61 RIALSPSPSLIGVDKIKYKCFRPRVRLITVLPELVEVRELVVQVDSVLEAD 120
 Qy 121 IRFAMRYLIDHDLFFPTVRVTEAEPLNNMGFRVDKVLKVSRRPELYGALPTLDEL 180
 Db 121 IRFAMRYLIDHDLFFPTVRVTEAEPLNNMGFRVDKVLKVSRRPELYGALPTLDEL 180
 Qy 181 RIALPDIIVSVKSGSPRRDPVTVYAVKTDQDEVRVIAKCDKDRPQIRNRYKVVYD 240
 Db 181 RIALPDIIVSVKSGSPRRDPVTVYAVKTDQDEVRVIAKCDKDRPQIRNRYKVVYD 240
 Qy 241 PDIVGNNHNDPMTLLRRARLIGIKLDVTRVGLPTTIVSHGVSVGVLNVLVDYA 300
 Db 241 PDIVGNNHNDPMTLLRRARLIGIKLDVTRVGLPTTIVSHGVSVGVLNVLVDYA 300
 Qy 301 EMPEIKIKLEVAETLVKMSKSRVINWMEIPDWDPKGKLLQAYADVATG 360
 Db 301 EMPEIKIKLEVAETLVKMSKSRVINWMEIPDWDPKGKLLQAYADVATG 360
 Qy 361 LAEKILPFAIQLSVYGLQDVGMSVGRLEWILIDAEFKSELVPRVVERPEITG 420
 Db 361 LAEKILPFAIQLSVYGLQDVGMSVGRLEWILIDAEFKSELVPRVVERPEITG 420
 Qy 421 AVLEPLAGVHENIADVSSPMYKINIKVGPDLVLRGEGCGEGWEAEVGRFR 480
 Db 421 AVLEPLAGVHENIADVSSPMYKINIKVGPDLVLRGEGCGEGWEAEVGRFR 480
 Qy 481 RCPGFFVTYLLERLELRNVEAKMKYPPDSPEYLLDRQALKVLANSYGVMSG 540
 Db 481 RCPGFFVTYLLERLELRNVEAKMKYPPDSPEYLLDRQALKVLANSYGVMSG 540
 Qy 541 ARWCQECANVTAMGRHLITKINTAKKGLKVIYGDYLSLPTDYSKVPYFKIKE 600
 Db 541 ARWCQECANVTAMGRHLITKINTAKKGLKVIYGDYLSLPTDYSKVPYFKIKE 600
 Qy 601 ELGFEIKLEVVYLLPFTAKYVAGLEQSDRIDVGFENVGWGCWELAKVQVNVIV 660
 Db 601 ELGFEIKLEVVYLLPFTAKYVAGLEQSDRIDVGFENVGWGCWELAKVQVNVIV 660
 Qy 661 LKTSKQKQVYKIVKELSESKQPIKSLVNTKLSLSEKVTSDHGVAKVMSG 720
 Db 661 LKTSKQKQVYKIVKELSESKQPIKSLVNTKLSLSEKVTSDHGVAKVMSG 720
 Qy 721 YVSGDKQKQVYKIVKELSESKQPIKSLVNTKLSLSEKVTSDHGVAKVMSG 780
 Db 721 YVSGDKQKQVYKIVKELSESKQPIKSLVNTKLSLSEKVTSDHGVAKVMSG 780

QY 777 FGITEKJ,KASATGOKTLEDFLAKK 801

Db 121 EADIFRANXILNDKLYPTTAVYBAENAGRSFGFVSQSVTVTVDEPFI -ADTISDI 178
 Qy 178 PLRLTALPFIIVISQSGSPRPDPVIVAVTDGDDGVFLIARQDKRPFIFPFTVK 237
 Db 179 FBNKYLAPFIIVISQSGSPRPDPVIVAVTDGDDGVFLIARQDKRPFIFPFTVK 238
 Qy 238 RYDPIIVGVNNHDPYLLIARLQIKQIDTTRVGAETTVISGHVSVGLANDLY 297
 Db 239 SDPPIIVGVNNHDPYLLIARLQIKQIDTTRVGAETTVISGHVSVGLANDLY 298
 Qy 298 DYBAEMPEIKIKLEAVLYGVWKKSKSVIMNMEITVDPKQFLLQVQADVRA 357
 Db 299 NYVBEHEIKIKLEAVLYGVWKKSKSVIMNMEITVDPKQFLLQVQADVRA 358
 Qy 358 TYGAKILPFIALQISVTVGLPQDVGANSVGLFVLYLDAFQKELVNNRVERPEET 417
 Db 359 TYGAKILPFIALQISVTVGLPQDVGANSVGLFVLYLDAFQKELVNNRVERPEET 418
 Qy 418 YGNAVLEPLGVNENLVNPMKINWGPDPVLVREKSGS -CSCWAPREV 476
 Db 419 YGNAVLEPLGVNENLVNPMKINWGPDPVLVREKSGS -CSCWAPREV 478
 Qy 477 HRFKPGSPFETULFELLEIKRYBAWKKYPPSPFVLELDFQKALKLVANAGY 536
 Db 479 HMFKPSGPFETULFELLEIKRYBAWKKYPPSPFVLELDFQKALKLVANAGY 538
 Qy 537 GMSAKNCRKCAVWAGWUHLTPRAVNAKGLKLVNODTLELTVNDRKNTK 596
 Db 539 GNVHNVKTCSEAVTAGNGLLSAETARKLAKLVIGDLSLVTVYDEKVKKLE 598
 Qy 597 ITKEELGPIKLEKTVLFTFAKRYVAGLELGGVNVGVNCGKALNAGVQVY 656
 Db 599 FVYKQGLFKIKGVNFTTEKRYKLVLLGGGMDVGVFVQDGLAKEVQK 658
 Qy 657 DVYVATSEVNAVETVILVLELSEKQVPIKLVNNTLSHLEETTVRQVNVANW 716
 Db 659 AELTNGDINALSTVREKLRKRGKIPITKLVNKTLLNIEVTEHAPVITASEM 718
 Qy 717 LSNAGTVSGDKIGTVVGGGRISORAMPTVMDQSQIDTVTVDDHITPALALY 776
 Db 719 KEGTDVQKGLVTVVGGGSSSRAPVYVIM -DSKKVUTVTVTVQVAVNRLY 777
 Qy 777 FQITEKGLKASQKGLFELAKK 801
 Db 778 FVTEKGLKASQKGLFELPAKK 802
 RESULT 13
 AAB19510
 AC AAB19510 standard; Protein; 785 AA.
 AC AAB19530;
 XX 09-JUN-2001 (first entry)
 XX Pyrobaculum islandicum DNA polymerase.
 DE Pyrobaculum islandicum DNA polymerase.
 XX DNA polymerase; 3'-5' exonuclease; thermostable; DNA amplification;
 XX DNA sequencing.
 XX Pyrobaculum islandicum.
 OS W0200053772.1.
 XX 14-SEP-2000.
 PD 14-SEP-2000.
 XX 04-MAR-2000; 2000MO-BP01917.
 PF 06-MAR-1999; 98EP-0104539.
 PR 02-SEP-1999; 98EP-0117245.
 XX (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX

Kaehler M, Frey B, Sobek H, Antranikian G;
 WF: 2000-58749/55.
 N-PSDB, AAB0678.
 Novel DNA polymerase of Pyrobaculum islandicum used for determining DNA
 sequences, comprising six conserved motifs indicative of family B DNA
 polymerases and possessing exonuclease activity -
 Disclosure; Fig 1/2; 38pp; English.
 The present sequence is that of the novel DNA polymerase of the
 archaeo hyperthermophilic Archaeon, Pyrobaculum islandicum DSM24184.
 The sequence was deduced from a DNA polymerase gene (see AAB0678).
 isolated from P. islandicum chromosomal DNA. The enzyme includes 6
 conserved motifs, indicating a family B DNA polymerase. The amino acid
 sequence of the P. islandicum DNA polymerase gene is shown. The
 gene was transformed by a vector including the P. islandicum gene is
 claimed. The P. islandicum DNA polymerase is thermostable, having a
 half-life of 30-40 min at 100 degree C and over 10 hr at 90 degree C.
 The enzyme can be used for determining DNA sequences. The enzyme also has 3'-5' proofreading
 exonuclease activity, providing a substantially lower base
 incorporation error rate than non-proofreading DNA polymerases.
 Sequence 785 AA;
 Query Match 50.8%; Score 2129.5; DB 21; Length 785;
 Best Local Similarity 53.4%; Pred. No. 2.2e-191;
 Matches 429; Conservative 141; Mismatches 195; Indels 39; Gaps 13;
 9 LDGSEVVGKGPQVIGLNGSERVILIDRSREVFY---ALLARGDPKVAQKRAL 65
 8 LDTTAVGVSVEIRFGLIUSGSRVILIDRSFPFPPVDCACEPA-----AKAL 60
 66 SRPKSPFICVDKRYKGPFRVLRITVLPFAVRYELVNVGVQDVEADREFAM 125
 61 SR-VAPIDVGVVRRFLRSGSKETAKTPEDEVLEKRAMSIFRVSGVTEADTFPM 119
 126 KYLIDHOLEPFTVVEASEPLENKGPRVDKV--VLATGSRPEPLVG--BALATPKLPDLR 181
 120 RYIMDGVVPCSNVAVER-----GRLGGIPTTVSQ-----MYGDSGFPF---LK 166
 182 TLADPTVSGPSPRPDPVIVAVTDGDDGVFLIARQDKRPFIFPFTVKVYVD 241
 167 WNAFIDVNERGSPDPDIPVQMLAKTNGHEVFEASCDRGVAVPFIETSDP 226
 242 DTNGNHNHPPHLLARLQIKQIDTTRVGAETTVISGHVSVGLANDLYADVA 301
 227 DTVGVNSGDPFPIVLESAAGVPLATD-RLSNFPQOSVYGRHSIVGRANVLNVE 285
 302 EHFETKLESEVARYTQNSKRSVIVNNMEITVDPKQFLLQVQADVRAVTVGL 361
 286 EPEFKLKTDEAVETVGVWKKSERVILPGKIVETWQDFNKELARYVLDVSTGL 345
 362 AKTLPALQISVTVGLPQDVGANSVGLFVLYLDAFQKELVNNRVERPEET 421
 346 ADMLPFLVGSNLSGLPQDVGANSVGRVWMLLEVATLGEVAPNRESEVEPIGA 405
 432 IVLEPAGVHNVNADLSNKPIMIKYNGPDTLVFPGKSGCCWAPREVRRFR 481
 406 IVLEPAGVHNVNADLSNKPIMIKYNGPDTLVFPGKSGCCWAPREVRRFR 465
 482 CPGGFTVLIERLEKKRYVAKMKKYPDPSFELDERQKALANASVGMNCSGA 541
 466 SPYGVQVQLVLEKLVKELKARERAKTTPDSPEFKLDERQKALANANATOLGV 525
 542 RYTCRCNAVNTANGRLIRTAIARLAKLVIGTQDLSFTYVDQKVENFKTKE 601
 526 RYTVREAVASTPAFALIMDVYIQARLALVYVYGDTSFLYKQSGD-VDKLKIVR 584
 602 LQPEIKLEVYKSELTFFETKRYKGLDEPRIDIVGEVAVGDMCELAKEVTVL 661
 Qy

Db 585 YGIDKNDQYAKVFTPEAKYAGLLAGRIDGVFVFNVGDSNLANQVQLRIEIL 644
 Qy 662 KTSFVNA-----VEYVKVKEIEBEKQVPELVKTKLSKLEKNTETPAVNAKQML 717
 Db 645 KSRDVEARHGVKTEIIRLRYKFNKFDLIIWTKLDELKDYAVPNNVAQLK 704
 Qy 718 SAGVRSGEDKIGTVYVKGGRISQRAWPFVNDQSDIVTVYDQITIPAALETIGTF 777
 Db 705 RIGVYVKGTVITVYVKGGRISQRAWPFVNDQSDIVTVYDQITIPAALETIGTF 764
 Qy 778 GTTKKLKASATG--QKTFDFPLA 799
 Db 765 GWGSDLR--TGRWSSLSLPLS 785

RESULT 14

1D AAY52022 standard; Protein; 781 AA.

AC XX AAY52022;
 AD 12-JUL-2000 (first entry)
 AC XX A. fulgidus AF0497 protein.
 DE A. fulgidus AF0497 protein.
 XX Polymerase; thermostable; nucleic acid elongation; sliding clamp protein;
 XX amplification, reverse transcription.
 XX Archaeoglobus fulgidus.
 OS Archaeoglobus fulgidus.
 XX DB1984071-AA.

PD 10-FEB-2000.

XX 07-SEP-1996; 9805-1040771.

XX 06-AUG-1998; 9805-1035653.

XX (LION-) LION BIOSCIENCE AG.

XX Voss H, Moeckel G, Xober I, Kilger C,
 XX WPI; 2000-207149/19.

XX A thermostable in vitro polymerase complex for template-dependent
 PT elongation of nucleic acids in amplification or reverse transcription
 PT methods -
 XX Disclosure; Page 72-75; 152pp; German.

XX This invention describes a novel thermostable in vitro complex for
 CC template-dependent elongation of nucleic acids which comprises a
 CC elongation protein that shows thermostable polymerase activity. The
 CC elongation protein in vitro accessory complex can be used to produce the
 CC thermostable in vitro complex, which is useful for template-dependent
 CC elongation of nucleic acids. For amplification of nucleic acids by the
 CC polymerase chain reaction or reverse transcriptase-polymerase chain
 CC reaction (RT-PCR). The complex can be used to mark nucleic acids.
 CC AAY52000-Y52084 and AAY9752-970799 represent proteins and protein
 CC fragments used to illustrate the method of the invention.

XX Sequence 781 AA;

Query Match 37.8%; Score 1591; DB 21; Length 781;
 Identity 42.5%; Similarity 42.5%; No. 1,3e+13;
 Matches 330; Conservative 133; Mismatches 273; Indels 68; Gaps 18;
 Qy 1 MTEVFTVLSDSEVWGEFQVINGIAENRERVLTREFFPFFVALLAGAPKQVQA 60
 Db 1 NERVESGVLIDNDETIGKAVELACDQDQ-IFVADYNDFPFTVI---GVYDEILKN 56

Qy 61 RIALSPKPSHIGVDEKQKFRFRVRVRLKTVLFAVREYBELVNVQVDEVDLEAD 120
 Db 57 ANISREYVTKLSFQIAQKATLQZVEGYSYVIANHVRQYKQADQIAQVG---VYRAD 113
 Qy 121 IFAPEAYLIDLDLFFETVFAEAPLENQG-----FRVKNVTVKSRPEPLVGEALAPT 175
 Db 114 KPAFRLVLDLQACGQIAIGE-----KQGVIVSTKIEKV-----ERIFPM 135
 Qy 176 KLPDRLAFDPDQSGQSPSPEDPVVIAVKTDDGVLFATSGDDKQKPIREBYV 235
 Db 158 EFPEKQVPCDMLSSGQPPEDCPPIVIVTNDDBETILG---DERKILSDPVKL 214
 Qy 236 VQYEDPDIIVGNWNEFQWLYRLARLGLKLDVTRVAGAPETTSVH--GNVSVGRLN 293
 Db 215 KISYDPIIVGNNDQAFDFPIVTKRAERNWTFD---VGRGSNVFGQRPVGRLN 270
 Qy 294 VQLYDPAENRPTKISLEFVAYLVGMKQSERVINHWRIPTQWDDPKRPLQLQVARD 353
 Db 271 VQLYDPAENRPTKISLEFVAYLVGMKQSERVINHWRIPTQWDDPKRPLQLQVARD 327
 Qy 354 VQRYKQYAKVLFALQVTCVGLDQVMSQSERVYLVTRANQVKEVLNVVER 413
 Db 328 DAINTYLAKELLPMWELSMITLFPVDVYTRMGKQVQMLSEACKIGETANPPEH 387
 Qy 414 PEYTRAVVAFERAGVHVAHVPKQSKNIMTKVNGDGLVPRGKQCEGQAP 473
 Db 388 -AESVEGAVLERGHEVACLDPASVPSMIANISDPTV-----QCD-DCTEAP 440
 Qy 474 EYQRPFRCPQGFITVLETLERVRAVMKQYPPSPFETLLDBQKALKVLAASV 533
 Db 441 EYQRPFRCPQGFITVLETLERVRAVMKQYPPSPFETLLDBQKALKVLAASV 500
 Qy 534 QYMGSGANWPCRAVATWGRHLINTAINAKGLKATYIGTDSLFTV---YDPRK 590
 Db 501 QYMGSGANWPCRAVATWGRHLINTAINAKGLKATYIGTDSLFTV---YDPRK 560
 Qy 591 VENFIKIKELQFEKLEKYKELFFTEKQRYAGLEEDRIDVGFRAVRGQWCEAK 650
 Db 561 VDLKDKHLELFQIEVDSITSAITPFE--KXITAGTIDQGLVYKGLVRGQWCEAK 619
 Qy 651 EVQTVKVEIATSEVNAEVVRKVELEBEKQVPELVKTKLSKLEKNTETPAHW 710
 Db 620 KQVREVLVLEPFAEPLASQVADVIRKQSGSERVYVYKQITKQSKIESQWAP 679
 Qy 711 VAKRSLASGVYSGDKIGTVYVKGGRISQRAWPFVNDQSDIVTVYDQITIPAA 785
 Db 680 KALAKAREGHIYVPSKIGTVYVKGGRISQRAWPFVNDQSDIVTVYDQITIPAA 739
 Qy 786 IDVTYVVDQITIPAAIRLQVIGTEKKLAKAQKQKTFDFPLA 799
 Db 740 LNDYVDINDQIPSVLAILERFGYTPALQSS--QMSLDSFFS 781

RESULT 15

1D AAY51651 standard; protein; 781 AA.

AC AAY51651;
 AC AAY51651;

DT 01-JUN-2000 (first entry)

DE A. fulgidus AF0497 protein fragment.

XX Thermostable; template-dependent elongation; aclepe protein;
 XX elongation protein; amplification; reverse transcription.
 OS Archaeoglobus fulgidus.

FN W0200008164-A2.

XX 17-FEB-2000.

XX 06-AUG-1999; 99NO-DS02480.

Db 181 RLTAEDIVTSQSGSPRDPVIVAVNDTDDDBVLTJABKQDQKREFFVETVD 240
 Qy 241 PDIVGNNHDPMTLLRLARLGLTGLVTRVQAEPTTSVGHVSVFORLMDLYDA 300
 Db 241 PDIVGNNHDPMTLLRLARLGLTGLVTRVQAEPTTSVGHVSVFORLMDLYDA 300
 Qy 301 EMBPEIKTSLSEVAVTLYGWMKSERVILNHWEPIDMDPKPDLLOIARDVSLTG 360
 Db 301 EMBPEIKTSLSEVAVTLYGWMKSERVILNHWEPIDMDPKPDLLOIARDVSLTG 360
 Qy 361 LAKBPLFALQSVTGLPUDQGVMSVGFLEMTLIRAFKMKELPNVPRPEPTTG 420
 Db 361 LAKBPLFALQSVTGLPUDQGVMSVGFLEMTLIRAFKMKELPNVPRPEPTTG 420
 Qy 421 AVLEPAGVGHENIADLSMTPIKNGDPTLVREKSGCGCBWAEVGRFR 480
 Db 421 AVLEPAGVGHENIADLSMTPIKNGDPTLVREKSGCGCBWAEVGRFR 480
 Qy 481 RCPGPFKTVLERLLELAKKVAEMKKYPPSPSEYLLDRBKOKALYANASGYMWSG 540
 Db 481 RCPGPFKTVLERLLELAKKVAEMKKYPPSPSEYLLDRBKOKALYANASGYMWSG 540
 Qy 541 ARWCECAVNAVJWGRHLITAINIARGLAVIYQDTSFVYDPRKVENFKIKE 600
 Db 541 ARWCECAVNAVJWGRHLITAINIARGLAVIYQDTSFVYDPRKVENFKIKE 600
 Qy 601 ELGPEIKLEKVEYLFETFAKSKYAGLLDGRDITVGEFAVWDCBLAKSVOTVVEIV 660
 Db 601 ELGPEIKLEKVEYLFETFAKSKYAGLLDGRDITVGEFAVWDCBLAKSVOTVVEIV 660
 Qy 661 LKTSVNNVAVETVKIYVKKGBRI SQRAWPFVMDQSDQDVTYVQHOITPAALRLGTFGIT 780
 Db 661 LKTSVNNVAVETVKIYVKKGBRI SQRAWPFVMDQSDQDVTYVQHOITPAALRLGTFGIT 780
 Qy 781 EKKJASATGOKTLDFDLAKSK 803
 Db 781 EKKJASATGOKTLDFDLAKSK 803

RESULT 2

US-09-948-369-4
 ; Sequence 4, Application US/09948369
 ; Patent No. US2002013243A1
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: CALLEN, Walter
 ; APPLICANT: MATHUR, Eric
 ; TITLE OF INVENTION: ENZYMS HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY AND METHODS C
 ; FILE REFERENCE: DIVER1350-3
 ; CURRENT APPLICATION NUMBER: US/09/948.369
 ; CURRENT FILING DATE: 2001-09-05
 ; PRIOR FILING DATE: 2000-09-06 US/07/656.309
 ; PRIOR APPLICATION NUMBER: US 09/391.340
 ; PRIOR FILING DATE: 1998-09-07
 ; PRIOR APPLICATION NUMBER: US 08/907.166
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 4
 ; TYPE: PNT
 ; ORGANISM: Pyrobolus fumarius
 ; US-09-948-369-4
 Query Match 100.0%; Score 4188; DB 10; Length 803;
 Best Local Similarity 100.0%; Pred. No. 0;

Matchee 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTSVPTVLDSSVEVCKEPQVINGIANGERRVILDRSEPRVYIATLAPGADQVQAQ 60
 Db 1 MTSVPTVLDSSVEVCKEPQVINGIANGERRVILDRSEPRVYIATLAPGADQVQAQ 60
 Qy 61 RTRALSRPSPITGVEDDKKRYKPRPRVRLTRVLPVAVRELVNVDGVDEVLAD 120
 Db 61 RTRALSRPSPITGVEDDKKRYKPRPRVRLTRVLPVAVRELVNVDGVDEVLAD 120
 Qy 61 RTRALSRPSPITGVEDDKKRYKPRPRVRLTRVLPVAVRELVNVDGVDEVLAD 120
 Db 61 RTRALSRPSPITGVEDDKKRYKPRPRVRLTRVLPVAVRELVNVDGVDEVLAD 120
 Qy 121 IFAPAMHLDHDLFFFTWRVZAPLEKNGRVDVQIVLVSRPELVGEALATPLGLD 180
 Db 121 IFAPAMHLDHDLFFFTWRVZAPLEKNGRVDVQIVLVSRPELVGEALATPLGLD 180
 Qy 181 RLTAEDIVTSQSGSPRDPVIVAVNDTDDDBVLTJABKQDQKREFFVETVD 240
 Db 181 RLTAEDIVTSQSGSPRDPVIVAVNDTDDDBVLTJABKQDQKREFFVETVD 240
 Qy 241 PDIVGNNHDPMTLLRLARLGLTGLVTRVQAEPTTSVGHVSVFORLMDLYDA 300
 Db 241 PDIVGNNHDPMTLLRLARLGLTGLVTRVQAEPTTSVGHVSVFORLMDLYDA 300
 Qy 301 EMBPEIKTSLSEVAVTLYGWMKSERVILNHWEPIDMDPKPDLLOIARDVSLTG 360
 Db 301 EMBPEIKTSLSEVAVTLYGWMKSERVILNHWEPIDMDPKPDLLOIARDVSLTG 360
 Qy 361 LAKBPLFALQSVTGLPUDQGVMSVGFLEMTLIRAFKMKELPNVPRPEPTTG 420
 Db 361 LAKBPLFALQSVTGLPUDQGVMSVGFLEMTLIRAFKMKELPNVPRPEPTTG 420
 Qy 421 AVLEPAGVGHENIADLSMTPIKNGDPTLVREKSGCGCBWAEVGRFR 480
 Db 421 AVLEPAGVGHENIADLSMTPIKNGDPTLVREKSGCGCBWAEVGRFR 480
 Qy 481 RCPGPFKTVLERLLELAKKVAEMKKYPPSPSEYLLDRBKOKALYANASGYMWSG 540
 Db 481 RCPGPFKTVLERLLELAKKVAEMKKYPPSPSEYLLDRBKOKALYANASGYMWSG 540
 Qy 541 ARWCECAVNAVJWGRHLITAINIARGLAVIYQDTSFVYDPRKVENFKIKE 600
 Db 541 ARWCECAVNAVJWGRHLITAINIARGLAVIYQDTSFVYDPRKVENFKIKE 600
 Qy 601 ELGPEIKLEKVEYLFETFAKSKYAGLLDGRDITVGEFAVWDCBLAKSVOTVVEIV 660
 Db 601 ELGPEIKLEKVEYLFETFAKSKYAGLLDGRDITVGEFAVWDCBLAKSVOTVVEIV 660
 Qy 661 LKTSVNNVAVETVKIYVKKGBRI SQRAWPFVMDQSDQDVTYVQHOITPAALRLGTFGIT 780
 Db 661 LKTSVNNVAVETVKIYVKKGBRI SQRAWPFVMDQSDQDVTYVQHOITPAALRLGTFGIT 780
 Qy 781 EKKJASATGOKTLDFDLAKSK 803
 Db 781 EKKJASATGOKTLDFDLAKSK 803

RESULT 3

US-09-948-369-14
 ; Sequence 14, Application US/09948369
 ; Patent No. US2002013243A1
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: CALLEN, Walter
 ; APPLICANT: MATHUR, Eric
 ; TITLE OF INVENTION: ENZYMS HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY AND METHODS
 ; FILE REFERENCE: DIVER1350-3
 ; CURRENT APPLICATION NUMBER: US/09/948.369
 ; CURRENT FILING DATE: 2001-09-05
 ; PRIOR FILING DATE: 2000-09-06 US/07/656.309
 ; PRIOR APPLICATION NUMBER: US 09/391.340
 ; PRIOR FILING DATE: 1998-09-07
 ; PRIOR APPLICATION NUMBER: US 08/907.166
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 4
 ; TYPE: PNT
 ; ORGANISM: Pyrobolus fumarius
 ; US-09-948-369-4

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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/391,340
; PRIOR FILING DATE: 1998-09-07
; PRIOR APPLICATION NUMBER: US 08/907,166
; PRIOR FILING DATE: 1998-09-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; TYPE: EST
; ORGANISM: Pyrobolus fumarius
US-09-948-369-14

Query Match 100.0%; Score 4188; DB 10; Length 803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEVVFVLDSSVEVGEKPEVINGIAENGSRVLDASRFPVYVALLAGADPKVAQ 60
Db 1 MTEVVFVLDSSVEVGEKPEVINGIAENGSRVLDASRFPVYVALLAGADPKVAQ 60

Qy 61 RTALSRKSPFIQGVDDKRYKGRPRVLRIRTVLEAVREYELVNVDGVDEVLAD 120
Db 61 RTALSRKSPFIQGVDDKRYKGRPRVLRIRTVLEAVREYELVNVDGVDEVLAD 120

Qy 61 RTALSRKSPFIQGVDDKRYKGRPRVLRIRTVLEAVREYELVNVDGVDEVLAD 120
Db 61 RTALSRKSPFIQGVDDKRYKGRPRVLRIRTVLEAVREYELVNVDGVDEVLAD 120

Qy 121 IFPMRYLIDHDLFPFTVRVVEASELENKGFVDVTVLXSRPFLYGEALAPTKLP 180
Db 121 IFPMRYLIDHDLFPFTVRVVEASELENKGFVDVTVLXSRPFLYGEALAPTKLP 180

Qy 121 IFPMRYLIDHDLFPFTVRVVEASELENKGFVDVTVLXSRPFLYGEALAPTKLP 180
Db 121 IFPMRYLIDHDLFPFTVRVVEASELENKGFVDVTVLXSRPFLYGEALAPTKLP 180

Qy 181 RTLAQDIYVSKQSFRPDPVIVAKVDGDEVLAFAGDKDKRPFREFVYVRVD 240
Db 181 RTLAQDIYVSKQSFRPDPVIVAKVDGDEVLAFAGDKDKRPFREFVYVRVD 240

Qy 181 RTLAQDIYVSKQSFRPDPVIVAKVDGDEVLAFAGDKDKRPFREFVYVRVD 240
Db 181 RTLAQDIYVSKQSFRPDPVIVAKVDGDEVLAFAGDKDKRPFREFVYVRVD 240

Qy 241 PDIIVGNHNFHFWLRLARLIGIKDQTVRGVGEFTTSVGHVSFGRLANVDLYA 300
Db 241 PDIIVGNHNFHFWLRLARLIGIKDQTVRGVGEFTTSVGHVSFGRLANVDLYA 300

Qy 301 EMEPEIKISLEVASYLGMWKSERVLNWEIPDYMDPKRLLQAYADVDVATG 360
Db 301 EMEPEIKISLEVASYLGMWKSERVLNWEIPDYMDPKRLLQAYADVDVATG 360

Qy 301 EMEPEIKISLEVASYLGMWKSERVLNWEIPDYMDPKRLLQAYADVDVATG 360
Db 301 EMEPEIKISLEVASYLGMWKSERVLNWEIPDYMDPKRLLQAYADVDVATG 360

Qy 361 LAEKLPALQISVTLGDLQVGMGVGFLENTLRAAFKMKELVPRVPEETATG 420
Db 361 LAEKLPALQISVTLGDLQVGMGVGFLENTLRAAFKMKELVPRVPEETATG 420

Qy 361 LAEKLPALQISVTLGDLQVGMGVGFLENTLRAAFKMKELVPRVPEETATG 420
Db 361 LAEKLPALQISVTLGDLQVGMGVGFLENTLRAAFKMKELVPRVPEETATG 420

Qy 421 AIVLEPGHENTIANLDSNPNIMIKYVGPDLTVRGKSGCGCWBAPEVGRFR 480
Db 421 AIVLEPGHENTIANLDSNPNIMIKYVGPDLTVRGKSGCGCWBAPEVGRFR 480

Qy 481 RCPGPGFTVLELRLAKRVAEMKYPDPSPSEYFLADSRQKALANASTGMWNSG 540
Db 481 RCPGPGFTVLELRLAKRVAEMKYPDPSPSEYFLADSRQKALANASTGMWNSG 540

Qy 481 RCPGPGFTVLELRLAKRVAEMKYPDPSPSEYFLADSRQKALANASTGMWNSG 540
Db 481 RCPGPGFTVLELRLAKRVAEMKYPDPSPSEYFLADSRQKALANASTGMWNSG 540

Qy 541 ARWCECAVATANGHRLHTAINARGLKAVTQDSLFTVDPKVENFKIKE 600
Db 541 ARWCECAVATANGHRLHTAINARGLKAVTQDSLFTVDPKVENFKIKE 600

Qy 541 ARWCECAVATANGHRLHTAINARGLKAVTQDSLFTVDPKVENFKIKE 600
Db 541 ARWCECAVATANGHRLHTAINARGLKAVTQDSLFTVDPKVENFKIKE 600

Qy 601 ELGPEIKELVNTLFFETAKRYAGLLEGGIDVGFGEAVGDGMLAKVCTKVIV 660
Db 601 ELGPEIKELVNTLFFETAKRYAGLLEGGIDVGFGEAVGDGMLAKVCTKVIV 660

Qy 601 ELGPEIKELVNTLFFETAKRYAGLLEGGIDVGFGEAVGDGMLAKVCTKVIV 660
Db 601 ELGPEIKELVNTLFFETAKRYAGLLEGGIDVGFGEAVGDGMLAKVCTKVIV 660

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RESULT 4
US-10-034-849-2
; Sequence 2, Application US/10014849
; Sequence 2, Application US/2003015106A
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: CALLEN, Walter
; INVENTOR: CALLEN, Walter
; TITLE OF INVENTION: ENZYMES HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY
; TITLE OF INVENTION: AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: DIVERS/150-2
; CURRENT FILING DATE: 2003-12-23
; CURRENT FILING DATE: US/09/034,849
; CURRENT FILING DATE: 2003-12-23
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: US/09/656,309
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 803
; TYPE: EST
; ORGANISM: Pyrobolus fumarius
US-10-034-849-2

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Query Match 100.0%; Score 4188; DB 14; Length 803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 661 LKTSSEVNAVEVRKIVLSECKQVTEKIVKTLVSEVSEVTEAPVHVNAKMSAG 720
Db 661 LKTSSEVNAVEVRKIVLSECKQVTEKIVKTLVSEVSEVTEAPVHVNAKMSAG 720
Qy 721 YVSPDKGIVYVWGSGRISQDAPVWPKVDSQIDVTVVYVHQIIPAAILGIFGIT 780
Db 721 YVSPDKGIVYVWGSGRISQDAPVWPKVDSQIDVTVVYVHQIIPAAILGIFGIT 780
Qy 781 EKKUASATGQNTLPPFLAKSK 803
Db 781 EKKUASATGQNTLPPFLAKSK 803

RESULT 5
US-10-034-621-2
; Sequence 2, Application US/10034621
; Publication No. US2002031997A1
; GENERAL INFORMATION: CORPORATION
; APPLICANT: DIVERS CORP
; APPLICANT: CALLEN, Walter
; APPLICANT: MATHER, Eric
; TITLE OF INVENTION: ENZYMES HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY
; TITLE OF INVENTION: THERMO
; TITLE OF INVENTION: THERMO
; FILE REFERENCE: DIVER1350-2
; CURRENT APPLICATION NUMBER: US/10/034, 621
; PRIOR APPLICATION NUMBER: US/09/656, 309
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; SEQ ID NO 2
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Pyrobolus fumarius
US-10-034-621-2

Query Match 100.0%; Score 4188; DB 14; Length 803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEVVFVLDSSSEVWGKPEVVIINGIANGSERVLLIDRESPFYFALLAGADKQVAA 60
Db 1 MTEVVFVLDSSSEVWGKPEVVIINGIANGSERVLLIDRESPFYFALLAGADKQVAA 60
Qy 61 RIALRSPKSPFIOWDDKRTKGRPRVLRITVLPAAVREVELVNVGVDEVLAD 120
Db 61 RIALRSPKSPFIOWDDKRTKGRPRVLRITVLPAAVREVELVNVGVDEVLAD 120
Qy 121 IRPAMVLLIDHDEFFPTVAVRPAEFLKNGKRVKIVLVSKEPPIYGEALAPTKLPDL 180
Db 121 IRPAMVLLIDHDEFFPTVAVRPAEFLKNGKRVKIVLVSKEPPIYGEALAPTKLPDL 180
Qy 181 RIALDIEVYKSGSPRESDPVIVIAVTDGDSVLFIAEKDKDKRTGSEVYKVD 240
Db 181 RIALDIEVYKSGSPRESDPVIVIAVTDGDSVLFIAEKDKDKRTGSEVYKVD 240
Qy 241 PDIIVGTNNHFWPILRRARLGKIDVTRVGAETPTSVGHVSVFGRANLVDTYA 300
Db 241 PDIIVGTNNHFWPILRRARLGKIDVTRVGAETPTSVGHVSVFGRANLVDTYA 300
Qy 301 BEWPEIKLSIEVAETLGWKKSERVILNWEIPDYWDPRKCPRLQYARDVATNG 360
Db 301 BEWPEIKLSIEVAETLGWKKSERVILNWEIPDYWDPRKCPRLQYARDVATNG 360
Qy 361 LAKKLPILQATLSVTCLPDIQGVMSVGFLEMLTIRAFPMCKELPVRVSEPTTG 420
Db 361 LAKKLPILQATLSVTCLPDIQGVMSVGFLEMLTIRAFPMCKELPVRVSEPTTG 420
Qy 421 AVLEPAGVHENIATVLSNPKPMIKYINGDPLTVRQKSGCGECWAEVGRER 480
Db 421 AVLEPAGVHENIATVLSNPKPMIKYINGDPLTVRQKSGCGECWAEVGRER 480

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Qy 481 RCPGPKGVKTLERLLLEKRVBAEMKCPDPSPEVLLDRQAKVLANASVQVWGS 540
Db 481 RCPGPKGVKTLERLLLEKRVBAEMKCPDPSPEVLLDRQAKVLANASVQVWGS 540
Qy 541 ARNYCSBKAKVATANGRHILFTANIKLGLKVIKYGTDSLTPTVDPKVNWIKIKE 600
Db 541 ARNYCSBKAKVATANGRHILFTANIKLGLKVIKYGTDSLTPTVDPKVNWIKIKE 600
Qy 601 ELAPGKIKSVYGLFFETSAKGVAGLEGRDIDVGFPAVGCWELAKENVCVETV 660
Db 601 ELGFEIKLEKVIYGLFFETSAKGVAGLEGRDIDVGFPAVGCWELAKENVCVETV 660
Qy 661 LKTSSEVNAVEVRKIVLSECKQVTEKIVKTLVSEVSEVTEAPVHVNAKMSAG 720
Db 661 LKTSSEVNAVEVRKIVLSECKQVTEKIVKTLVSEVSEVTEAPVHVNAKMSAG 720
Qy 721 YVSPDKGIVYVWGSGRISQDAPVWPKVDSQIDVTVVYVHQIIPAAILGIFGIT 780
Db 721 YVSPDKGIVYVWGSGRISQDAPVWPKVDSQIDVTVVYVHQIIPAAILGIFGIT 780
Qy 781 EKKUASATGQNTLPPFLAKSK 803
Db 781 EKKUASATGQNTLPPFLAKSK 803

RESULT 6
US-10-029-382-2
; Sequence 2, Application US/10029382
; Publication No. US20020164618A1
; GENERAL INFORMATION: CORPORATION
; APPLICANT: DIVERS CORP
; APPLICANT: CALLEN, Walter
; APPLICANT: MATHER, Eric
; TITLE OF INVENTION: ENZYMES HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY
; TITLE OF INVENTION: THERMO
; TITLE OF INVENTION: THERMO
; CURRENT APPLICATION NUMBER: US/10/029,382
; PRIOR APPLICATION NUMBER: US/09/656,309
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; SEQ ID NO 2
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Pyrobolus fumarius
US-10-029-382-2

Query Match 100.0%; Score 4188; DB 14; Length 803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEVVFVLDSSSEVWGKPEVVIINGIANGSERVLLIDRESPFYFALLAGADKQVAA 60
Db 1 MTEVVFVLDSSSEVWGKPEVVIINGIANGSERVLLIDRESPFYFALLAGADKQVAA 60
Qy 61 RIALRSPKSPFIOWDDKRTKGRPRVLRITVLPAAVREVELVNVGVDEVLAD 120
Db 61 RIALRSPKSPFIOWDDKRTKGRPRVLRITVLPAAVREVELVNVGVDEVLAD 120
Qy 121 IRPAMVLLIDHDEFFPTVAVRPAEFLKNGKRVKIVLVSKEPPIYGEALAPTKLPDL 180
Db 121 IRPAMVLLIDHDEFFPTVAVRPAEFLKNGKRVKIVLVSKEPPIYGEALAPTKLPDL 180
Qy 181 RIALDIEVYKSGSPRESDPVIVIAVTDGDSVLFIAEKDKDKRTGSEVYKVD 240
Db 181 RIALDIEVYKSGSPRESDPVIVIAVTDGDSVLFIAEKDKDKRTGSEVYKVD 240
Qy 241 PDIIVGTNNHFWPILRRARLGKIDVTRVGAETPTSVGHVSVFGRANLVDTYA 300
Db 241 PDIIVGTNNHFWPILRRARLGKIDVTRVGAETPTSVGHVSVFGRANLVDTYA 300
Qy 301 BEWPEIKLSIEVAETLGWKKSERVILNWEIPDYWDPRKCPRLQYARDVATNG 360
Db 301 BEWPEIKLSIEVAETLGWKKSERVILNWEIPDYWDPRKCPRLQYARDVATNG 360

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Db 301. ERMPEKIKLSLEVAETLGVWKKSERVILNMEIPIYHODPKPQLLOIYARDVATYG 360
 361. LARKLPPALQSLVYGLPLQGVGMSVGEFLEIIRAFAPKELVHVRVERPESTYG 420
 Qy 361. LARKLPPALQSLVYGLPLQGVGMSVGEFLEIIRAFAPKELVHVRVERPESTYG 420
 Db 421. AVUEPLRGHENTIAVDLSFSPYIMIKVINGPDTLVRGKCKOCCHWAPKVEKFR 480
 Db 481. RCPGFFFTVLSRELLLEKLRVRAEMWKYPPSPVTELLDEROKALKUANASTGTMGSG 540
 Qy 481. RCPGFFFTVLSRELLLEKLRVRAEMWKYPPSPVTELLDEROKALKUANASTGTMGSG 540
 Db 541. RCPGFFFTVLSRELLLEKLRVRAEMWKYPPSPVTELLDEROKALKUANASTGTMGSG 540
 Qy 541. RCPGFFFTVLSRELLLEKLRVRAEMWKYPPSPVTELLDEROKALKUANASTGTMGSG 540
 Db 601. EGFETIKLEKVEKLEFFAKKXAGLEBGRDIVGEFAVGMCELANGVQVVEIV 660
 Qy 601. EGFETIKLEKVEKLEFFAKKXAGLEBGRDIVGEFAVGMCELANGVQVVEIV 660
 Db 661. EGFETIKLEKVEKLEFFAKKXAGLEBGRDIVGEFAVGMCELANGVQVVEIV 660
 Qy 661. EGFETIKLEKVEKLEFFAKKXAGLEBGRDIVGEFAVGMCELANGVQVVEIV 660
 Db 720. YRVSODKIGIVYKVGGRISQAMPYFVWQSDQIVTYVHDTLPAAIRLIGFGIT 780
 Qy 720. YRVSODKIGIVYKVGGRISQAMPYFVWQSDQIVTYVHDTLPAAIRLIGFGIT 780
 Db 781. EKKKASATQCKTLFDFLAKSK 803
 Qy 781. EKKKASATQCKTLFDFLAKSK 803
 Db 781. EKKKASATQCKTLFDFLAKSK 803

RESULT 7
 US-09-948-369-16
 ; Sequence 16, Application US/0948369
 ; Patent No. US20020134531
 ; GENERAL INFORMATION:
 ; APPLICANT: DIVERSA CORPORATION
 ; APPLICANT: CALLEN, Walter
 ; TITLE OF INVENTION: Elic
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: DIVER1350-3
 ; CURRENT APPLICATION NUMBER: US/09/948.369
 ; PRIOR APPLICATION NUMBER: US/09/656.309
 ; PRIOR FILING DATE: 2006-09-06
 ; PRIOR FILING DATE: 2006-09-06
 ; PRIOR FILING DATE: 1999-09-07
 ; PRIOR FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 803
 ; TYPE: PRT
 ; ORGANISM: Pyrobolus fumarius
 US-09-948-369-16

Query Watch 99.4%; Score 4164; DB 10; Length 803;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 797; Conservative 1; Mismatches 0; Gaps 0;

Qy 1. MTEVVTFTVLSVYVGVGSPVVIINGTAEKSERVILDSRPFFVYALLAGADPKVQAQ 60
 Db 1. MTEVVTFTVLSVYVGVGSPVVIINGTAEKSERVILDSRPFFVYALLAGADPKVQAQ 60
 Qy 61. RITALSRKSPCTICDQDKKCPKPRVLRATETVLPBAVRESELYKGVGVDEVLAD 120

Db 61. RITALSRKSPCTICDQDKKCPKPRVLRATETVLPBAVRESELYKGVGVDEVLAD 120
 Qy 121. ITPFAMTLIDHDFUFTFTVYVSEAPSPLENOGRFVOMYNTLVNSRPPELYGEALATPKLPDL 180
 Db 121. ITPFAMTLIDHDFUFTFTVYVSEAPSPLENOGRFVOMYNTLVNSRPPELYGEALATPKLPDL 180
 Qy 181. RILAFDIEVSEKSGSPRPDPVIVIAKTDGDEVLFTASGDOKRPIREFVEYVGYD 240
 Db 181. RILAFDIEVSEKSGSPRPDPVIVIAKTDGDEVLFTASGDOKRPIREFVEYVGYD 240
 Qy 240. RILAFDIEVSEKSGSPRPDPVIVIAKTDGDEVLFTASGDOKRPIREFVEYVGYD 240
 Db 241. POLIVGNNHHPDMPFLTLRLARLIGLITDVTGRVGLSEFTTVSHGVHVGSLNLDLYDA 300
 Qy 300. BEMPEIKLSLEVAETLGVWKKSERVILNMEIPIYHODPKPQLLOIYARDVATYG 360
 Db 360. BEMPEIKLSLEVAETLGVWKKSERVILNMEIPIYHODPKPQLLOIYARDVATYG 360
 Qy 361. LARKLPPALQSLVYGLPLQGVGMSVGEFLEIIRAFAPKELVHVRVERPESTYG 420
 Db 420. LARKLPPALQSLVYGLPLQGVGMSVGEFLEIIRAFAPKELVHVRVERPESTYG 420
 Qy 421. AVUEPLRGHENTIAVDLSFSPYIMIKVINGPDTLVRGKCKOCCHWAPKVEKFR 480
 Db 480. AVUEPLRGHENTIAVDLSFSPYIMIKVINGPDTLVRGKCKOCCHWAPKVEKFR 480
 Qy 481. RCPGFFFTVLSRELLLEKLRVRAEMWKYPPSPVTELLDEROKALKUANASTGTMGSG 540
 Db 540. RCPGFFFTVLSRELLLEKLRVRAEMWKYPPSPVTELLDEROKALKUANASTGTMGSG 540
 Qy 541. RCPGFFFTVLSRELLLEKLRVRAEMWKYPPSPVTELLDEROKALKUANASTGTMGSG 540
 Db 541. RCPGFFFTVLSRELLLEKLRVRAEMWKYPPSPVTELLDEROKALKUANASTGTMGSG 540
 Qy 601. EGFETIKLEKVEKLEFFAKKXAGLEBGRDIVGEFAVGMCELANGVQVVEIV 660
 Db 660. EGFETIKLEKVEKLEFFAKKXAGLEBGRDIVGEFAVGMCELANGVQVVEIV 660
 Qy 661. EGFETIKLEKVEKLEFFAKKXAGLEBGRDIVGEFAVGMCELANGVQVVEIV 660
 Db 661. EGFETIKLEKVEKLEFFAKKXAGLEBGRDIVGEFAVGMCELANGVQVVEIV 660
 Qy 720. YRVSODKIGIVYKVGGRISQAMPYFVWQSDQIVTYVHDTLPAAIRLIGFGIT 780
 Db 780. YRVSODKIGIVYKVGGRISQAMPYFVWQSDQIVTYVHDTLPAAIRLIGFGIT 780
 Qy 781. EKKKASATQCKTLFDFLAKSK 803
 Db 781. EKKKASATQCKTLFDFLAKSK 803

RESULT 8
 US-09-391-340-6
 ; Sequence 6, Application US/0931140A
 ; Patent No. US20020134531
 ; GENERAL INFORMATION:
 ; APPLICANT: Callen, Walter
 ; APPLICANT: Callen, Walter
 ; TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF NOVEL POLYMERASES
 ; FILE REFERENCE: 09410/027001
 ; CURRENT APPLICATION NUMBER: US/09/391.340A
 ; CURRENT FILING DATE: 1999-09-07
 ; PRIOR APPLICATION NUMBER: US/08/907.166
 ; EARLIER FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 803
 ; TYPE: PRT
 ; ORGANISM: Archaeoglobus lithotrophicus
 US-09-391-340-6

Query Match 37.3%; Score 1563; DB 9; Length 768;

Best Local Similarity 41.3%; Pred. No. 1.8e-135;
Matches 338; Conservative 154; Mismatches 273; Indels 54; Gaps 18;

Qy 1 MTEVPTVLDSVSGSPQVITVIAKVTDDGDEVTASGDKDRKFRFVYK 60
Db 1 MTKYGMILLADITENDGAVRLKCKDEG--IFATATDSFPYFALKKEGITADIVYK 59

Qy 61 -RIRALGRKPEKIPEDDGRKQFPRVLRITVLPEAVRELVGVGVGVLEA 119
Db 60 IKVCKKEVITP-LKVEETAKNGRVEVYARHPQVPAKRVGQ--YLEIRA 115

Qy 120 DTRFAMZITDHLFPPTVTVVABP-ENNGRFRVDKVIYK--SRPEPVGELAPFL 177
Db 116 DIFPAPVTLDSKACHGVITGVREK-SUKCTEIKETRSQD-----F 163

Qy 178 PDLRLAPDEVISQSPSPQVITVIAKVTDDGDEVTASGDKDRKFRFVYK 237
Db 164 PELKAVPDCMLSEVMDPEKDPFIIVISKSGVEYL--NGDNREBELUTFKIR 220

Qy 238 RYDDIIVGVNNHDPVILARRARLIGKIDVTRKGAETTVSGVGVGRGLVLY 297
Db 221 DTDIDPVLGVGDSFPMPTKGRKAKVLYDGR--DESELAIRGRPKIAGLVLY 278

Qy 298 DVAEMKPEKIGLEVAVLGVKWSERVILNMELDPYDDPKRQLQVARDVLA 357
Db 279 DLAMSGLVKKLNLNAPLG--KILKELDENDIYHRTS--GRDSVYKTSQDILN 335

Qy 358 TYGLAKELFALQISVYGLDQVGMVSGVLELWILRAAFKMKELVNRPEEST 417
Db 336 TYFABELLPMHLSMIRIPLDVTGSGRQKVEMLSEAKGLAPRRFN--AUS 394

Qy 418 YGAVLPELGVGHEINAVLDSSPMIMKTNVGDPTLVPRGKCGCGCHAEPEVH 477
Db 395 YEGAFPLGAGLHNVCLDPSANPSTKINISDPLV--GKDCDGN--APBVG 450

Qy 478 RPRCPGPFVTLLELLEKRVKAEKMKYFDSSEFVELDGRQALKYLANASVIG 537
Db 451 KXPHGDPGFRLKMLIKRRETKKVMKTLDTNBFYGLDTKQATLVNSFGTGG 510

Qy 538 NSGAWYCECAVATANGHRLITAINAKGLKIVYDGLSFLVYDKEVNFYK 597
Db 511 NMLAKWYCECAVATANGHRLITAINAKGLKIVYDGLSFLVYDKEVNFYK 570

Qy 598 IK-----BELCPLEKLVKRYKFPFTAKRYAGLAEQRIIDVGVKGVGDCLEAK 650
Db 629 IKQWYCECAVATANGHRLITAINAKGLKIVYDGLSFLVYDKEVNFYK 609

Qy 651 EVQYKVEVLKVEVMAVYKRVLEKQFVETKLVTKLSKRLSEYTFEAPY 710
Db 630 KIQWYCECAVATANGHRLITAINAKGLKIVYDGLSFLVYDKEVNFYK 689

Qy 711 VAARWMSAGVTVSGKQIVYVKGGRISQAPMPFWVD-----PSQIDV 758
Db 759 TYDQVQIIPAAKRLGVFTKLSKASQKQTLDF 797

Qy 759 TYDQVQIIPAAKRLGVFTKLSKASQKQTLDF 797
Db 750 EYIDVQVLESVTLERFGTEAQKGAEE--QQTLDAP 787

RESULT 9

US-09-948-369-6
Sequence 6; Application US/09940369
General Information: US/09940369
General Information: US/09940369
Applicant: DIVERSA CORPORATION
Applicant: CALLEN, Walter
Title of Invention: ENZYMES HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY AND METHODS C
Title of Invention: THEREOF
File Reference: DIVER1350-3
Current Application Number: US/09/940-369
Current Filing Date: 2001-09-06

Prior Application Number: US 09/456,309
Prior Filing Date: 2000-09-06
Prior Application Number: US 09/391,340
Prior Filing Date: 1999-09-07
Prior Application Number: US 08/907,166
Prior Filing Date: 1997-06-06
Number of SEQ ID NOS: 16
Software: Patent in version 3.0
SEQ ID NO: 788
TYPE: PRT
ORGANISM: Archaeoglobus lithotrophicus
US-09-948-369-6

Query Match
Best Local Similarity 41.3%; Pred. No. 1.8e-135;
Matches 338; Conservative 154; Mismatches 273; Indels 54; Gaps 18;

Qy 1 MTEVPTVLDSVSGSPQVITVIAKVTDDGDEVTASGDKDRKFRFVYK 60
Db 1 MTKYGMILLADITENDGAVRLKCKDEG--IFATATDSFPYFALKKEGITADIVYK 59

Qy 61 -RIRALGRKPEKIPEDDGRKQFPRVLRITVLPEAVRELVGVGVGVLEA 119
Db 60 IKVCKKEVITP-LKVEETAKNGRVEVYARHPQVPAKRVGQ--YLEIRA 115

Qy 120 DTRFAMZITDHLFPPTVTVVABP-ENNGRFRVDKVIYK--SRPEPVGELAPFL 177
Db 116 DIFPAPVTLDSKACHGVITGVREK-SUKCTEIKETRSQD-----F 163

Qy 178 PDLRLAPDEVISQSPSPQVITVIAKVTDDGDEVTASGDKDRKFRFVYK 237
Db 164 PELKAVPDCMLSEVMDPEKDPFIIVISKSGVEYL--NGDNREBELUTFKIR 220

Qy 238 RYDDIIVGVNNHDPVILARRARLIGKIDVTRKGAETTVSGVGVGRGLVLY 297
Db 221 DTDIDPVLGVGDSFPMPTKGRKAKVLYDGR--DESELAIRGRPKIAGLVLY 278

Qy 298 DVAEMKPEKIGLEVAVLGVKWSERVILNMELDPYDDPKRQLQVARDVLA 357
Db 279 DLAMSGLVKKLNLNAPLG--KILKELDENDIYHRTS--GRDSVYKTSQDILN 335

Qy 358 TYGLAKELFALQISVYGLDQVGMVSGVLELWILRAAFKMKELVNRPEEST 417
Db 336 TYFABELLPMHLSMIRIPLDVTGSGRQKVEMLSEAKGLAPRRFN--AUS 394

Qy 418 YGAVLPELGVGHEINAVLDSSPMIMKTNVGDPTLVPRGKCGCGCHAEPEVH 477
Db 395 YEGAFPLGAGLHNVCLDPSANPSTKINISDPLV--GKDCDGN--APBVG 450

Qy 478 RPRCPGPFVTLLELLEKRVKAEKMKYFDSSEFVELDGRQALKYLANASVIG 537
Db 451 KXPHGDPGFRLKMLIKRRETKKVMKTLDTNBFYGLDTKQATLVNSFGTGG 510

Qy 538 NSGAWYCECAVATANGHRLITAINAKGLKIVYDGLSFLVYDKEVNFYK 597
Db 511 NMLAKWYCECAVATANGHRLITAINAKGLKIVYDGLSFLVYDKEVNFYK 570

Qy 598 IK-----BELCPLEKLVKRYKFPFTAKRYAGLAEQRIIDVGVKGVGDCLEAK 650
Db 629 IKQWYCECAVATANGHRLITAINAKGLKIVYDGLSFLVYDKEVNFYK 609

Qy 651 EVQYKVEVLKVEVMAVYKRVLEKQFVETKLVTKLSKRLSEYTFEAPY 710
Db 630 KIQWYCECAVATANGHRLITAINAKGLKIVYDGLSFLVYDKEVNFYK 689

Qy 711 VAARWMSAGVTVSGKQIVYVKGGRISQAPMPFWVD-----PSQIDV 758
Db 759 TYDQVQIIPAAKRLGVFTKLSKASQKQTLDF 797

Qy 759 TYDQVQIIPAAKRLGVFTKLSKASQKQTLDF 797
Db 750 EYIDVQVLESVTLERFGTEAQKGAEE--QQTLDAP 787

Db 437 GCEYDVAQVGHKCKCFDFFPSLGLLEERQVQKQKKA-TIDPEKLLDQRA 485
 Qy 525 LVANASVGVMSGASGYCBACAKAVANGHILHTAL-NIARKGLKVIYGTDSL 583
 Db 486 IKLANLFGYGT 545
 Qy 584 VYDSEKNTVNIKILSELG-----SILKEVTELEFTEAKGYVGLLEORID 634
 Db 546 ATPGDNDVTVKAKPEFQYDYNALPOLLSELEFTEGTGTGTGTGTGTGTGT 604
 Qy 635 IVGFAVGVDMICLAEQCKVHVHLKTSVKNVAVKIVLESEKPTTEKLVNWK 694
 Db 605 TGLSIVREMSVETDARVLAHLGDSVGEAVIVKIVTELSKIVTEPELVTE 664
 Qy 695 TUSLKGLELITTEAHVAVKASGVSGDKVIVKVGGRISORAMPVNVDPDS 754
 Db 665 QTRDLDKATPHAVAKELAGKIKIRPQVIVSYLVKSGSRIGDRAIP-FQEDPDA 723
 Qy 755 --QIDVTVVDRHITPAALRILGVFTTEKLGKASATQNTLFOPLAKNS 802
 Db 734 KIKYDARYHNIENVULFAVERILAFRQYKEDQVAKTRVGLGVAWAKPNT 773
 RESULT 12
 US-10-227-110-67
 ; Application US/10227110
 ; Publication No. US20030143577A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Strategene
 ; FILE REFERENCE: 25436/2155C
 ; CURRENT APPLICATION NUMBER: US/10/227,110
 ; CURRENT FILING DATE: 2002-08-23
 ; PRIOR FILING DATE: 2002-09-29, 241
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: 10/208,508
 ; PRIOR FILING DATE: 2002-07-30
 ; PRIOR FILING DATE: 2002-07-30
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.1
 ; LENGTH: 775
 ; TYPE: PAT
 ; ORGANISM: Pyrococcus sp.
 US-10-227-110-67
 Query Match 29.81; Score 1248; DB 121; Length 775;
 Best Local Similarity 36.11; Pred. No. 2,7e+106;
 Matches 301; Conservative 134; Mismatches 281; Indels 98; Gaps 22;
 Qy 8 VLSVSEVGVGSEPOVINGANGSEVVLIDSEFFVALLAGADQKV-----AQIR 63
 Db 2 ILMDUTITEQNTIRFK-KENGEFQVYVNERFVYALLAQDSQIDSEVKITABHG 60
 Qy 64 ALSPEKSPGIDGGKQVGGPRVIRIVTFAVRELVGVGVGVLENDF 123
 Db 61 KIVR-----ILDKAKRKFAGHTEFWRLVFEHPQVPAIRKIRHSVADTFPYDIFP 116
 Qy 124 ARVYLIDLPFTTVVFEAEPLNKGPRVDVYLVKSRPELVGSALEKLPULRIL 183
 Db 117 ARVYLIDKGLI-----FMECD-----SEMLKL 138
 Qy 184 AFDVLEVYSGSPREDPVIIVATIDGDEVL-----FPAKGDKRQKIFREYV 235
 Db 139 AITGKIDKLELHES-EPNKGIDVIMSYADREDAVYVWKIDLPFVVSSEHMKLAKY 197
 Qy 236 VKRVDYLDIHWGNNHMDVPLLRALRILKIDVTRVGEAFTSVIGHL--VEVPEGL 292
 Db 198 IREQVDDVITITNGDSFLPILVAKELGILQALPADG-GSEFQKQGVQGVNTVWIKAI 256
 Qy 293 NVLDVTVASENPEIKSLSEVASYGVGMKSERVILWMEITPQVDPKSPFLQVAYR 352

Db 257 HPDLVTVHRTINFTTEVTEAL-FQPEKNTAN-----EIANSTQKGLERAKVSM 313
 Qy 353 DVYAVTGLAKLIPALQVGVVGLDQVAGSVBRLVTLPAAPQKMLVPAHVE 412
 Db 314 DGLAVTELGFEQVAGVAGVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 373
 Qy 413 RPE-----BTGATGLVLEKRWHEINAVUSPSSKIVNIVKIVGVTLVPEQKOE 466
 Db 374 ERYERHLSVAGAVVPEKGLMGVLSFSSPS111THVSPDTAME-----427
 Qy 467 GCGWS--APEVGHRTFCGFVKVLELLEKREVALENKYPDESPFVALLDERQK 523
 Db 428 -AGRVAVVGVGKFCDFPFSFISLKLRLDERKEIKERA-SKDPTEKONDIQOR 582
 Qy 524 ALKLVANASVGVMSGASGYCBACAKAVANGHILHTAL-TAINIARKGLVYGTDSL 583
 Db 486 AKILANLFGYGT 545
 Qy 583 PTV---DFKVB---NFTKILSELG--FELKSNVTVLPTEAKGYVGLLEORID 633
 Db 546 YATPGDNDVTVKAKPEFQYDYNALPOLLSELEFTEGTGTGTGTGTGTGTGT 604
 Qy 634 DIVGFAVGVDMICLAEQCKVHVHLKTSVKNVAVKIVLESEKPTTEKLVNWK 693
 Db 605 TGLSIVREMSVETDARVLAHLGDSVGEAVIVKIVTELSKIVTEPELVTE 664
 Qy 694 KTLGKLELITTEAHVAVKASGVSGDKVIVKVGGRISORAMPVNVDPDS 752
 Db 665 BOTPMLHFKATGHPHVAKELAGKIKIRPQVIVSYLVKSGSRIGDRAIP-SR 721
 Qy 753 --PSQIDVTVVDRHITPAALRILGVFTTEKLGKASATQNTLFOPLAKNS 803
 Db 722 DAREKDYHNIENVULFAVERILAFRQYKEDQVAKTRVGLGVAWAKPNT 775
 RESULT 13
 US-10-208-508-67
 ; Application US/10208508
 ; Publication No. US20030180741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Strategene
 ; FILE REFERENCE: 25436/2155B
 ; CURRENT APPLICATION NUMBER: US/10/208,508
 ; CURRENT FILING DATE: 2003-05-07
 ; PRIOR FILING DATE: 2002-09-29, 241
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: 10/035,091
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 67
 ; LENGTH: 775
 ; TYPE: PAT
 ; ORGANISM: Pyrococcus sp.
 US-10-208-508-67
 Query Match 29.81; Score 1248; DB 12; Length 775;
 Best Local Similarity 36.11; Pred. No. 2,7e+106;
 Matches 301; Conservative 154; Mismatches 281; Indels 98; Gaps 22;
 Qy 8 VLSVSEVGVGSEPOVINGANGSEVVLIDSEFFVALLAGADQKV-----AQIR 63
 Db 2 ILMDUTITEQNTIRFK-KENGEFQVYVNERFVYALLAQDSQIDSEVKITABHG 60
 Qy 64 ALSPEKSPGIDGGKQVGGPRVIRIVTFAVRELVGVGVGVLENDF 123
 Db 61 KIVR-----ILDKAKRKFAGHTEFWRLVFEHPQVPAIRKIRHSVADTFPYDIFP 116
 Qy 124 ARVYLIDLPFTTVVFEAEPLNKGPRVDVYLVKSRPELVGSALEKLPULRIL 183
 Db 117 ARVYLIDKGLI-----FMECD-----SEMLKL 138

; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: 10/208,508
 ; PRIOR FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: 10/035,091
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 29
 ; LENGTH: 773
 ; TYPE: PRT
 ; ORGANISM: Thermococcus gorgonarius
 US-10-227-110-29

Query Match 29.74; Score 1245.5; DS 12; Length 773;
 Similarity 96.86%; Mismatches 146; Minmatches 289; Gaps 21;
 Matches 300; Conservative 146;

QY 8 VLDSSVVGQZVQVINGIANKSERVLLIRFPFPIALLARGA---DPOV-AQRIR 63
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 QY 64 ALGSPKPILOVDDEKRTFSPKRVLRKTVLEAVRETELVKQVQDVQVLEADIKF 123
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 61 TVVA---VDSERVKKNFLQPTVWKVLFPHQDVPAINDKIKHPNAVIVYDIPF 116
 QY 124 NAYLIDHIDLPFTWVRKAEPLKNGKGFVKVYVWSRPEPIVGEALPTKLPDRL 183
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 117 ASYLLDQGLI-----PWGD-----ELANWL 138
 QY 184 AFDIVYSKQSRFRSDPPIVIAKVDQDQVYL-----FIAGQDDKQPIREFVY 235
 DB 1 AFDITLTHESFAR-GPILMISVADSGARVITKKNIDLPVQVWSEKSLRFLK 197
 QY 236 VARYDDIVVNNRHPDPTLLRPARILKIDVTRVQAEPTYSVGR---VSVQGL 292
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 198 VAEQDPVLTITNGDFNALKKSEKLGTF-ILGEBSPEYQKQMGDFAEVQGR 255
 QY 293 NVLDYVASEWEPKIKSIEVAYLGWKKSERVLIIMWEIPIQDPKGFLLQYAR 352
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 257 HDPLVPIRTINLPITTLNVETAI FQPK-EKYAB--ELAQWETGRLVARTSM 313
 QY 353 DUVANTYGLAKLIPFALQSLVYVGLPQDYGMSVGFLEWILYIAAFKMGELVNR-- 410
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 314 EDKVTTELQKEFFMEQLSLVQSLNDVSRSTGSLVNFLLANAYELNLRKFD 373
 QY 411 ---VRFETIRALVLEPFLQWENAVLDFSSNFMIMINWQDPILOVRPCKQCB 467
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 374 ERELARSTAGQVKEPEKLMNVILDFSLVPSIITNNVSDPLNR----- 426
 QY 468 QMG---AFYQKPRCPQFQKTVLELRLELRVRAEMKYPSPSPFLLEBQKA 524
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 427 GCEYDVANQGNKCFQFIPSLGLDLERQVKKQMA-TIDPEKLLVLRQA 485
 QY 525 LKYNANSTGMSNGNNTCEANATANGRLIRTI-MIARKGLAYITGTSLF 583
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 486 KILANSEFTGTGAATACGASWANGVQETTRIEKQKVALTDGFF 543
 QY 584 VYDEKPVNTIILIELF-----EILEKYKGLFFFAKQVAGLQDQID 634
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 546 ATTPGADSVKKAKEFLDYINKLPGLELEPIESFNGFFV-TKKXVATDEDKIT 604
 QY 635 IVGNAVQDCELANQVKNVYIKTSVMAVVRKIVLEKEKQVPELVNKK 694
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 605 TGLGLEIVMSSEIANQKRVLLALKGQDSEAVLVKSTKSKVPELVNYY 664
 QY 695 TLAKSELTETEAHVAAQKMGASQVSGKIGVYKQGRISQAMPFNVQDPS 754
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 665 QTRDLNQTAKTCHVAVALAANGIKIRKQTVISYVLAASSRIGQATP-FDEIPA 723
 QY 785 --QIVYTVDDHILPALRIIGVHGTETKKAATQKTLFPIAKS 802
 DB 1 LUTDYITDEKQVIRFK-KENGEPKIDYDSFEYIYALKDSALEVDKXITARRG 60
 DB 724 KRYQDAETIENQVLAVERLLKAVKYNEDYKQKTRQGLQWAKPT 773